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A Study Evaluating Genetic Trends and Molecular Predisposition to Improved Carcass Quality of Brahman and Brahman Influenced Cattle

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A STUDY EVALUATING GENETIC TRENDS AND MOLECULAR PREDISPOSITION TO IMPROVED CARCASS QUALITY OF BRAHMAN AND BRAHMAN INFLUENCED CATTLE

A Thesis

Submitted to the Graduate Faculty of the
Louisiana State University and
Agricultural and Mechanical College
in partial fulfillment of the
requirements for the degree of
Master of Science

in

The Department of Animal Sciences

by
Amanda Michelle Royer
B.S., Louisiana State University, 2011
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ABSTRACT

The first objective of the current study was to evaluate genetic trends from 10 years of the American Brahman Breeders Association Carcass Evaluation Program from 2004 to 2013. Changes of performance in growth, carcass composition, and carcass quality traits were evaluated. Overall means were calculated to report the total average for each trait along with an average rate of change per year. Growth traits evaluated included feedlot entrance weight (INWT), harvest weight (HRVWT), and average daily gain (ADG). Carcass composition and quality traits evaluated included hot carcass weight (HCW), rib eye area (REA), marbling score (MARB), dressing percent (DP), quality grade (QG), yield grade (YG), and Warner-Bratzler shear force score (WBS). Trends indicated that over the 10 year period of improved sire selection, Brahman cattle began entering the feedlot lighter, exited heavier, and improved average daily gain. Furthermore, all carcass composition and quality traits showed overall improvement with the exception of shear force scores. Further investigation of shear force score showed WBS had in fact been experiencing a favorable downward trend since 2009.

The second objective of this study was to evaluate SNP located on six candidate genes and their potential association with growth, carcass composition, and carcass quality traits in a population of Brahman and Brahman-influenced steers that participated in the ABBA carcass evaluation program. Traits analyzed included birth weight (BW), weaning weight (WW), hip height (HH), days on feed (DOF), and the previously mentioned feedlot and carcass traits INWT, HRVWT, ADG, HCW, REA, MARB, DP, QG, YG, and WBS. Single nucleotide polymorphisms (SNP) were chosen for analysis within six candidate genes including Thyroglobulin (TG, Adiponectin (ADIPOQ), Calpastatin (CAST), Calpain-3 (CAPN3), Insulin like growth factor-1 (IGF1), and Growth Hormone gene (GH1). Analysis revealed representation

of all six candidate genes in the 41 SNP found to have 58 significant associations ($p<.05$) with growth and feedlot traits BW, WW, HH, INWT, HRVWT, DOF, and ADG. Furthermore, all six candidate genes were represented in the 32 SNP found to have 49 significant associations with carcass composition and quality traits HCW, REA, YG, MARB, QG, and WBS. No markers showed association with DP.

CHAPTER I
INTRODUCTION

Improvement in the Brahman breed has been sought after for some time now, as can be seen through the participation by producers in the American Brahman Breeders Association Carcass Evaluation Program. Brahman cattle have reportedly produced less tender meat, lower marbling scores, and lower carcass quality grades as opposed to *Bos taurus* cattle. (DeRouen et al, 2014; Wheeler et al, 2001). Because sire selection can affect the performance of a herd as a whole, the ABBA worked with producers to help them realize the impact of sire selection on economically important traits. The research presented here evaluated feedlot growth traits, carcass composition, and carcass quality traits of Brahman and Brahman influenced steers participating in the ABBA carcass evaluation program. Growth traits included feedlot entrance weight (INWT), harvest weight (HRVWT), and average daily gain (ADG). Carcass composition and quality traits included hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), yield grade (YG), quality grade (QG), dressing percent (DP), and Warner-Bratzler shear force score (WBS).

The identification and use of molecular markers has been used to increase the rate of genetic improvement in economically important traits in beef cattle (Davis et al, 1998). Using candidate genes of known physiological function to evaluate single nucleotide polymorphisms (SNP) allows analysis of potential associations with economically important traits. This is especially useful for lowly heritable traits, and traits that are difficult to measure. The current study evaluated SNP located on six candidate genes and their potential association with growth, carcass composition, and carcass quality traits in a population of Brahman and Brahman-influenced steers. The candidate genes chosen included Adiponectin (ADIPOQ), Thyroglobulin (TG), Calpain 3 (CAPN3), Calpastatin (CAST), Insulin like Growth Factor 1 (IGF1), and Growth Hormone gene (GH1). The candidate genes utilized were previously reported to be associated with growth and carcass traits (Mullen et al., 2010; Pereira et al., 2005; Machado et al., 2003; Casas et al., 2005; Schenkel et al., 2006; Koohmaraie et al., 2002; Barendse et al., 1999). Traits used in analysis included birth weight (BW), weaning

weight (WW), hip height (HH), days on feed (DOF), and the previously mentioned traits entrance weight (INWT), harvest weight (HRVWT), average daily gain (ADG), hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), yield grade (YG), quality grade (QG), dressing percent (DP), and Warner-Bratzler shear force (WBS).

CHAPTER II
REVIEW OF LITERATURE

Performance Testing

Historically, centralized performance bull tests has been utilized as a tool for producers to evaluate young bulls' performance that may be introduced as herd sires. Centralized performance testing allows a group of bulls to be evaluated solely based upon performance in a uniform environment. Comparisons among test subjects are made possible through a standard testing environment, regardless of differences in cattle such as management background or breed (Auchtung et al., 2001). Prior to the testing process, the Beef Improvement Federation has suggested cattle be afforded a 21-day adjustment period to become accustomed to their new environment and diet (BIF, 2010). This time period allows for compensatory gain to take place, which is characterized by a more rapid weight gain after a period of restricted nutrition (Sainz et al.,1995). Because compensatory gain does not appear in test data, the centralized performance tests allow cattle to showcase their individual growth ability and productivity between weaning and yearling age through uniform evaluation (Auchtung et al 2001).

Data is collected on bulls every 28 days for the duration of the 112-day test in order to evaluate the individual growth curve of each animal. The growth and production traits typically evaluated include average daily gain (ADG), 112 day weight, feed-to-gain ratio, weight per day of age, yearling hip height, and carcass ultrasound data are measured and/or calculated (Simpson et al, 1986; BIF, 2010). Scrotal circumference (SC) is also measured due to its relationship with age at puberty (Cammack et al., 2009), and age at first calving (Martínez-Velázquez et al, 2003).

As Wheeler and associates (1997) reported, no single breed excels in all traits that are important to beef production, thus diversity is needed to develop and utilize heterosis and breed complementarity in the many

different facets of the beef industry (Wheeler et al, 1997). Performance testing provides a method to select sires best suited for specific types of beef cattle operations.

Genetic trends in beef cattle

Genetic improvement directly results from selection and breeding specifically aimed at promoting improvements in breed performance attributes (Garrick et al., 2009). Thus, identifying and understanding the additive genetic merit of livestock is key to improving subsequent generations of beef cattle through replacement breeding animals (Golden et al, 2009). Through various national cattle evaluation programs and breed associations, producers have increased accuracy of selection using technologies available to them such as breed-specific performance indices or economic indices (Bullock et al., 2009)(Garrick et al., 2009).

Improvement of economically important traits can be seen through the evolution of genetic trends in British cattle as reported by MacNeil and Northcutt in 2008. The study reported an increase in standardized breeding value for marbling score, rib eye area, and subcutaneous fat depth from 1990 to 2006 through analysis of postslaughter data collection.

A second study evaluated trend improvement in the beef industry, including analysis of growth traits of Brahman cattle from 1968 to 1996 (Plasse et al., 2002). Through specific selection methods aimed at improving growth performance over a 30 year period, positive phenotypic changes were observed in growth traits including birth weight, 205-d weaning weight and 18 month weight. Furthermore, Thornton and associates reported (2010) that due to improved genetic selection, global beef production has more than doubled since the 1960s, and carcass weights have increased by 30 percent.

Carcass Characteristics

Carcass traits are collected to measure carcass composition, yield, and quality. Carcass composition traits include hot carcass weight (HCW), rib eye area (REA), backfat thickness, intramuscular fat (IMF), and kidney, pelvic, and heart fat (KPH). Carcass yield traits include dressing percent, and yield grade. Carcass

quality traits evaluated include quality grade (QG), marbling score, and meat tenderness via Warner-Bratzler Shear Force measurement (WBS).

Carcass composition traits are measured during harvest along the disassembly line. Hot carcass weight is measured directly after evisceration and hide removal, but before chilling or any further carcass processing. Rib eye area is measured between the 12th and 13th rib, as is backfat thickness and marbling score. KPH fat in the visceral cavity is measured as a percentage of hot carcass weight upon removal from the carcass during disassembly.

Yield Grade is a reflection of the amount of boneless closely trimmed retailed cuts (BCTRC) in a carcass, and is also called cutability. The formula uses HCW, backfat thickness, KPH fat, and ribeye area to assign a number between 1 and 5. The lower the numerical value of the USDA YG, the higher the yield of BCTRC. A carcass with a YG of 5 contains the most fat, least muscle, and is less desirable from a retail standpoint, expecting less than 45% BCTRC. A carcass with a YG 1 is the leanest, most trim carcass, and expects a yield of greater than 52% BCTRC. The industry average is around a YG 3, expecting between 47.5% and 50% BCTRC (Hale et al., 2007).

Dressing percentage (DP) is a reflection of the amount of carcass in relation to live weight, and is calculated by dividing HCW by live weight, and multiplying by 100. The average DP for a steer is 62% (USDA, 1997).

Marbling scores are assigned based on the amount of intramuscular fat observed in the ribeye after the hanging carcass has been ribbed between the 12th and 13th rib. This measurement is further utilized to calculate a carcass quality grade. Marbling score ranges include devoid, traces, slight, small, modest, moderate, slightly abundant, moderately abundant, and abundant. These are used in conjunction with carcass maturity to assign a USDA Quality Grade. Quality Grades range from worst quality to best quality as follows: Utility, Commercial, Standard, Select, Choice, and Prime. (Hale et al., 2007)(USDA, 1997)

Another component to palatability of carcasses is meat tenderness, which is measured using a Warner-Bratzler shear force instrument. This requires a process of preparing and cooking steaks, then extracting core samples from the cooked steaks to be sheared perpendicular to muscle fiber direction (Silva et al., 2014). With this test, the amount of force required to shear through each core sample is measured in kilograms. A lower measurement equates to more tender core samples than higher scored, tougher core samples (Wheeler et al., 1998).

In recent years, the U.S. Department of Agriculture (USDA) has collaborated with beef industry leaders in academia and the private sector to develop a tenderness system similar to that of the Quality Grading system of Prime, Choice, Select, etc. The objective was to establish thresholds for beef to be marketed as USDA Certified Tender or USDA Certified Very Tender based upon shear force values of the longissimus dorsi, or ribeye muscle, using the Warner-Bratzler (WBSF), or Slice Shear Force (SSF) reading (www.ams.usda.gov). Minimum Tenderness Threshold Values (MTTV) were set for USDA Tender and USDA Very Tender beef. The MTTV for USDA Tender was set at 4.4kg WBSF or 20.0kg SSF. The threshold for USDA Very Tender beef was set as 3.9kg for WBSF or 15.3kg for SSF. In 2012, the Agriculture Marketing Service sector of the USDA began collaborating with segments of the industry to implement the new Tenderness Marketing Claim at the retail level (www.ams.usda.gov). Companies may request approval to use the USDA Certified Tender claim, and once approved, may promote their meat products as USDA-Certified Tender or Very Tender using product labeling and marketing.

Genetic markers

Genetic marker technologies are being utilized to aid in improved selection and product improvement. A genetic marker is a DNA sequence mutation within an individual's genome, and can be utilized in investigating genetic variations between individuals (Yang et al., 2013). Genetic markers have a definite physical location on a gene and may be inherited together. These markers may have no known function. According to the National

Human Genome Research Institute (NHGRI), genetic markers can be used to identify and track the inheritance of a gene that has not been identified yet but whose approximate location is known to be near the genetic marker. Three of the most common genetic markers utilized are microsatellites, single nucleotide polymorphisms, and restriction fragment length polymorphisms (RFLP) (Yang et al., 2013). Yang and associates (2013) reported that utilization of RFLP's was first developed by Grodzicker et al. in 1974 and was utilized to identify mutations among individuals through DNA fragments of varying size, that were generated through the use of known restriction enzymes. Microsatellites are short tandem repeats in the DNA sequence commonly between one and six base pairs, repeated in tandem several times through a DNA strand (Litt et al., 1989). Microsatellites are used in paternity testing for a multitude of species including in beef production (McClure et al., 2012). The repetition of microsatellites in DNA allows for identification of regions that may harbor genes or mutations associated with performance traits. Finally, a single nucleotide polymorphism (SNP) is defined by the National Human Genome Research Institute as a single nucleotide base change at a specific location in a DNA sequence. An SNP may be in the form of an insertion, deletion, transition, or transversion (Yang et al., 2013; Vignal et al., 2002). The DNA bases are read in triplets to determine which amino acids will be produced in a specific location, therefore SNPs have the ability to alter the amino acids being made (Crawford et al., 2005). Single Nucleotide Polymorphism association studies aim to evaluate SNPs as a possible source of variation, and whether that variation has an effect on whether an animal is pre-disposed to superior or inferior performance in an economically important trait (Yang et al., 2013).

Quantitative Trait Loci

Quantitative trait loci (QTL) are specific regions on a chromosome containing genes or mutations that may be responsible for variation in economically important traits. A quantitative trait is a phenotypic trait which can be measured numerically. Genetic markers and linkage maps have aided in identification of QTLs associated with traits of economic importance (Casas et al., 2000). For example, QTL affecting carcass quality

and composition traits have been previously mapped to chromosomes 1, 2, 5, 13, and 14 (Stone et al., 1999). Mapping QTLs depends on the genetic dominant or recessive nature of the trait, heritability of the trait, and the number of genes affecting the trait (Members of the Complex Trait Consortium, 2003). In addition, mapping accuracy depends on marker distribution throughout the genome, so the efficiency of QTL mapping also relies on large numbers of markers per chromosome (van Ooijen et al., 1992). Using QTLs in genetic selection may improve selection for economical traits in other technologies such as marker assisted selection or whole genome selection (Andersson et al., 2001; Soller et al., 1983).

Marker Assisted Selection

Marker Assisted Selection (MAS) is the process of utilizing genetic markers that have been associated with economically important quantitative traits. This has the potential to allow for early and accurate identification of animals that are genetically predisposed to have increased performance for economically important traits. Through early identification of these individuals, producers may decrease costs associated with raising and performance testing inferior animals (BIF, 2010). When comparing MAS to the use of Expected Progeny Differences (EPDs) or phenotypic selection, the rate of improvement via MAS may increase especially in those traits deemed lowly heritable (Davis et al., 1998). Through the use of genotyping technologies, MAS would decrease the amount of time producers would typically have to wait to apply selection strategies in the beef production process, such as early detection of superior animals for tenderness or marbling (Lu et al., 2013; Macneil et al., 2001). Marker Assisted Selection is most useful when the marker accounts for the highest degree of variation for the evaluated trait. Rocha and associates (1992) further reported that if genetic markers associated with genetic variability can be identified and selected for, then selection accuracy can be increased. However, this increased level of performance is influenced by numerous variables.

One variable that must be considered is the number of markers. Too few markers may result in a low power to detect any significant effect, whereas too many markers may result in low significance levels for any

one marker (Davis et al., 1998). An optimum number of markers allow for maximum response to be returned. Additionally, the interaction of markers associated with quantitative traits and the level of heritability of the trait must be considered to improve accuracy of selection (Davis et al., 1998).

Whole Genome Selection

Whole Genome Selection (WGS) is a selection tool utilizing all markers known to account for variability within a trait. Whole Genome Selection is similar to Marker Assisted Selection, with the exception that WGS uses all identified genetic markers associated with a trait spanning the entire genome whereas MAS only utilizes a small number of associated markers (Goddard et al., 2007). Furthermore, WGS can result in a large improvement in selection accuracy compared to parental average breeding values (Lu et al., 2013). Thallman reported (2009) that there are a larger amount of genes with small phenotypic effects throughout the genome, than there are genes with large phenotypic effects. Whole Genome Selection uses all associated markers, emphasizes regions with more effect, thereby accounting for more genetic variation (Thallman, 2009). In the cattle industry, WGS is used in harnessing large amounts of data and predicting genetic merit values (Matukumalli et al., 2009). Goddard et al (2007) credit the practicality of WGS to new methods to efficiently genotype large numbers of single nucleotide polymorphisms. This implementation of new and existing technologies can increase animal selection accuracy, and aid producers in lowering financial expenditure and economic risk due to poor selection (Harris, 1998).

Single Nucleotide Polymorphisms

A single nucleotide polymorphism (SNP) is a single nucleotide base change at a specific location in a DNA sequence. Deoxyribonucleic acid bases include adenine, cytosine, guanine, and thymine. Single base changes, insertions, and deletions are all types of SNPs (Vignal et al., 2002). Single Nucleotide Polymorphism association studies aim to evaluate SNPs as a possible source of variation, and whether that variation has an effect on whether an animal is pre-disposed to superior or inferior performance in an economically important

trait (Yang et al., 2013). Identification of SNPs associated with economically important traits could lead to an understanding of the predisposition of certain individuals to perform differently. For example, Page and associates (2002) reported SNPs on bovine CAPN1 associated with variation in meat tenderness in a population of crossbred cattle. Using SNPs in genetic selection may improve selection for economical traits in other technologies such as candidate gene approach (Magee et al., 2010).

Candidate Gene

A candidate gene is a gene of known physiological function and has previously described association with a specific trait of interest (NHGRI). Candidate genes can be utilized when testing for association with complex traits in which genes have small effects on the complex trait (Karisa et al., 2013). Candidate genes can be identified using numerous approaches including linkage studies, gene expression studies, and genome wide association studies. Large QTL regions may harbor candidate genes thought to have large effects on economically important traits (Saatchi et al., 2014). Identifying a single nucleotide polymorphism (SNP) within a gene can be used to narrow the region of interest on the gene. The variant may be the direct cause of the change, or could be in linkage disequilibrium with the gene that is the cause of the alteration (Tabor et al., 2002).

Thyroglobulin Gene

Thyroglobulin (TG) gene, located in the centromeric region upstream from the promoter on bovine chromosome 14, encodes the glycoprotein precursor to thyroid hormones (Wood et al., 2006). A polymorphism in the 5' promoter region of the bovine Thyroglobulin gene (TG5) has been associated with marbling variations in beef cattle (Casas et al., 2005). Cattle homozygous or heterozygous for the Thiamine (T) allele showed higher marbling scores than cattle homozygous for Cytosine (C) allele (Barendse et al., 1999). Brahman cattle showed lower frequencies of the favorable T allele, and lower marbling scores than their *Bos taurus*

counterparts (Casas et al., 2005). Casas et al reported (2005) that there is a lack of evaluation of these markers with carcass composition traits in *Bos indicus* cattle outside of their study.

Adiponectin Gene

The Adiponectin gene (ADIPOQ) is located on *Bos taurus* autosome 1, in close proximity to a QTL associated with carcass traits such as marbling, ribeye area, and backfat thickness (Morsci et al., 2006). Adiponectin modulates lipid and glucose metabolism, energy homeostasis, inhibits lipogenesis, acts as an anti-atherogenic agent, and is a neoglucogenic inhibitor (Morsci et al., 2006; Shin and Chung, 2013). It has been reported that expression of adiponectin by white adipose tissue into the bloodstream is negatively correlated with adipose tissue mass (Kadowaki et al., 2005; Morsci et al., 2006). Fatty acid presence and composition of adipose tissue associated with meat are important to meat quality and palatability (Kelly et al., 2014). Previous research showed two SNP significantly associated with increased ribeye area and backfat thickness in Hanwoo cattle (Shin and Chung, 2013). Adiponectin has also been reported to play a role in bone biology (Berner et al., 2004). Oshima and associates (2005) reported adiponectin increased bone mass in rats by suppressing osteoclastogenesis and activating osteoblastogenesis. The association between adiponectin and bodily processes indicate ADIPOQ as a promising candidate gene for further research with growth, carcass quality and composition traits.

Calpastatin Gene

The Calpastatin (CAST) Gene is located on *Bos taurus* autosome 7 (BTA7), and has been reported as a candidate gene for beef tenderness. Miller et al (1995) reported that tenderness is the most important trait to consumers in regards to meat quality. The CAST gene has been associated with calpastatin, a protein that inhibits the normal tenderization of meat as it ages postmortem (Shenkel et al., 2006). Calpastatin inhibits calpain, and regulates muscle cell protein proteolysis, thus its association with meat tenderness. While Calpain accelerates protein breakdown, Calpastatin inhibits it in post-mortem protein degradation (Koohmaraie et al.,

2002). Shackelford and associates reported (1995) this Calpain-Calpastatin complex plays a role in the ability of Brahmans to thrive in adverse conditions, but results in tougher meat as compared to comparable meat from *Bos taurus* cattle. Café and associates reported (2010) the favorable CAST allele was associated with lower Warner-Bratzler shear force scores in steaks from Brahman cattle. Higher frequency of the favorable allele showed a lower percentage of tough steaks but also increased fat and decreased rib eye area (Shenkel et al., 2006).

Calpain Gene

Calpain III (CAPN3) is located on BTA10. Of over a dozen isoforms of calpain, CAPN3 is the only isoform that is specific to skeletal muscle tissue (http://www.ncbi.nlm.nih.gov). A previously reported variant in the CAPN3 gene causes loss of catalytic activity of CAPN3 gene (Kramerova et al., 2004). Koohmaraie and associates reported (2002) that proteolytic degradation of myofibrillar proteins cause weakening of myofibrils and thus tenderization of meat in beef cattle. Calpain is responsible for the breakdown of myofibrillar protein (Wheeler and Koohmaraie, 1994), and plays a role in differentiation of preadipocytes to adipocytes (Patel et al., 1999), which are both closely related to meat tenderness. Calpastatin (CAST) inhibits calpain activity, thus regulating postmortem proteolysis (Schenkel et al., 2006).A previously reported polymorphism in the CAPN3 gene was found to be more common in zebu cattle than taurine cattle, which may contribute to the variation in tenderness in zebu or tropically adapted composite cattle (Barendse et al., 2008).

Insulin-like Growth Factor 1 Gene

The Insulin-like Growth Factor gene (IGF1) has been mapped to BTA5 (Grosse et al., 1999). Insulin-like growth factor is a protein hormone in the somatomedin family, which is synthesized and released by target tissues, mainly the liver, upon stimulation by growth hormone. As a result, insulin-like growth factor is considered a somatotropin-dependent somatomedin (Bauman, 1992). Machado and associates (2003) investigated an association of the IGF1 gene with growth traits including birthweight, weaning weight, and yearling weight in Canchim cattle. Islam and associates (2009) reported a significant association in an IGF1

SNP and varying fat content in Angus cattle. Angus cattle with the 'CC' genotype showed a higher fat depth and lower lean meat yield than cattle with the 'TT' genotype.

Growth Hormone Gene

Directly or indirectly, growth hormone (GH) is the main regulator of postnatal growth, including cell division, skeletal growth and protein synthesis (Curi et al., 2005; Trenkle and Topel, 1978). Synthesis of the protein hormone GH by somatotroph cells on the anterior pituitary is stimulated by growth hormone releasing hormone (GHRH) from the hypothalamus (Bauman, 1992; Trenkle and Topel, 1978). Growth hormone targets the liver where Insulin-like Growth Factor 1 (IGF1) is released and plays a role in tissue partitioning and nutrient use (Bauman, 1992). It has been previously described that the use of somatotropin increases muscle tissue accretion in growing animals (Etherton et al, 1998). The growth hormone gene (GH1) is located on BTA19 and has been previously associated with traits including growth and carcass quality (Pereira et al., 2005; Mullen et al, 2010). Previous reports suggest GH1 mutations are associated with varying levels of GH found in plasma, indicating GH1 as a candidate gene for improvement in various growth and carcass traits (Mullen et al., 2010)

Bos indicus / Brahman characteristics

Beef cattle production in subtropical regions of the United States must rely on cattle that can maintain a high level of performance for economically important traits under hot and humid climatic conditions (Elzo et al., 2012). *Bos indicus* and *Bos indicus* influenced cattle have been important to the U.S. and global beef industries due to their adaptability to heat and parasite stresses, which would limit *Bos taurus* productivity (Turner, 1980; Lyons et al., 2014; Thrift and Thrift, 2003).

Historically, animal performance was considerably enhanced by inclusion of *Bos indicus* breeds in a crossbred animal in subtropical climates (Garrick et al., 2009). Crossing Brahman with *Bos taurus* contributes to reproductive and maternal advantages of crossbred cows (Franke et al., 2001). Elzo and associates (2011)

reported purebred Brahman cattle exhibited higher dressing percents, lower intramuscular fat content, smaller ribeye area, contained more connective tissue and was less tender beef, whereas Brahman/*Bos taurus* cross showed increase in ribeye area, fat over the ribeye, intramuscular fat, and hot carcass weight. However high proportions of Brahman inheritance tend to be less tender and have lower carcass quality grades than cattle with less Brahman influence (Smith et al., 2009).

Brahman cattle tend to have a delayed age at puberty, less intramuscular fat, and less tender beef as compared with *Bos taurus* breeds (Herring et al, 1996; Wheeler et al., 1990). *Bos indicus* cattle have been previously described as also having delayed maturity and longer gestation lengths than *Bos taurus* breeds (Wheeler et al., 2005). Understanding factors that affect these traits such as rate of maturity could thereby aide in the identification of the optimal genetic variants needed for beef cattle production in specific environments and systems. (Luna-Nevarez et al., 2010). For example, *Bos indicus* heifers reach puberty at an older age than *Bos taurus* heifers, and scrotal circumference of bulls is a trait reported to be favorably associated with heifer age at puberty (Eler et al., 2004; Brinks et al., 1978).

CHAPTER III
AN EVALUATION OF TEN YEARS OF CARCASS AND FEEDLOT PERFORMANCE IN BRAHMAN AND BRAHMAN INFLUENCED STEERS TESTED BY THE AMERICAN BRAHMAN BREEDERS ASSOCIATION (ABBA) NATIONAL CARCASS EVALUATION PROGRAM

Introduction

Brahman cattle are an economically important breed globally and are extensively utilized in beef production systems in tropical and sub-tropic regions. The breed's popularity is due to their parasite resistance and ability to tolerate hot, humid environments (Lyons *et al.*, 2014). However, Brahman and Brahman-influenced cattle have been reported to produce less tender meat (DeRouen *et al.*, 2014), exhibited lower marbling scores, and yielded lower carcass quality grades as compared to *Bos taurus* breeds (Wheeler *et al.*, 2001).

Cammack *et al.* reported (2009) that sire selection affects performance of the herd as a whole. Beginning in 2004 the American Brahman Breeders Association (ABBA) made a concerted effort to improve the growth traits, carcass quality, and composition traits of Brahman and Brahman-influenced cattle. The ABBA has collaborated with producers to help them realize the impact of sire selection on carcass quality traits, including meat tenderness, through data gathered from the ABBA Carcass Evaluation Program. The Carcass Evaluation Program has provided an excellent avenue for educating cattle producers on breed improvement through proper selection practices. By incorporating superior cattle into breeding programs and improving culling practices based on progeny feedlot performance, these efforts show that improvements may be made on a breed-wide basis in traits that have proven to be advantageous for the Brahman breed.

The objective of the current study was to evaluate genetic trends from 10 years of the ABBA Carcass Evaluation Program for 10 traits including growth, carcass composition, and carcass quality traits.

Materials & Methods

The steers were nominated in the Carcass Evaluation Program by the producer, and therefore the steers were subjected to specific background guidelines such as birthdate and lineage, and completed the health program outlined by ABBA prior to entrance into the feedlot. Steers from the program were evaluated for 10 traits, including growth, carcass composition, and carcass quality traits. Growth traits assessed included Feedlot entrance weight, harvest weight, and average daily gain. Carcass composition traits included hot carcass weight, dressing percent, rib eye area, and marbling score. Carcass quality traits analyzed were Quality Grade, Yield Grade, and Warner-Bratzler Shear Force for meat tenderness analysis.

Experimental Animals

Performance data was evaluated from 10 years of data from 2004-2013 provided by the American Brahman Breeders Association (ABBA) Carcass Evaluation Program. A total of 595 Brahman steers were nominated by beef cattle producers from across southeastern United States and evaluated in the current study.

A set of requirements set forth by ABBA must be met by producers wishing to participate in the ABBA Carcass Evaluation Program. Steers must be able to be registered by ABBA and must be born between January and May, must be weaned and have completed the ABBA outlined health program to enhance immunity and increase resistance to viruses, bacteria, and respiratory problems. The health program includes vaccination, de-worming, castration, and dehorning protocols, and must be completed 45 to 60 days prior to delivery to Graham Land & Cattle Company in Gonzales, Texas.

Upon arrival to Graham feedyard, steers are individually identified, processed, and weighed for an entrance weight (INWT). Steers are sorted into groups based on weight, frame size, and body condition before beginning on feed. Steers remain in feedlot for a period of time until feedyard manager determines harvest weight (HRVWT) has been reached. Using entrance weight, harvest weight, and number of days on feed, average daily gain (ADG) is calculated as amount of weight gain per day on feed.

At the conclusion of the feeding period, steers are sent to Sam Kane Beef Processors in Corpus Christi, Texas for harvest. Carcass composition and quality traits are collected and recorded. Composition and quality traits include hot carcass weight (HCW), rib eye area (REA), marbling score, dressing percent, quality grade, yield grade, and Warner-Bratzler shear force (WBS) as a measure of meat tenderness.

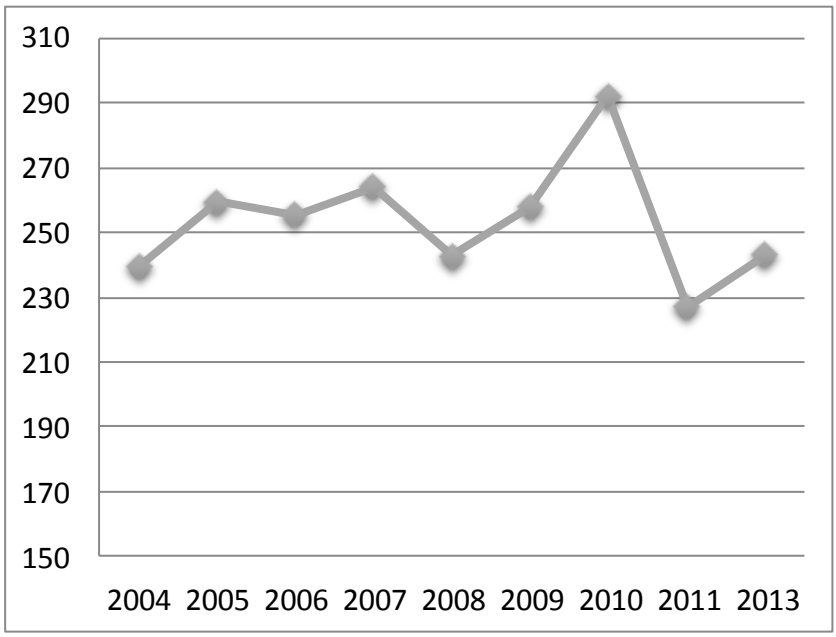
Statistical Analysis

The regression analysis procedures of SAS (version 9.2, SAS Institute, Cary, NC) were utilized to evaluate rate of positive or negative change of performance in each trait per year for steers nominated in the Carcass Evaluating Project from 2004 to 2013. Entrance weight (InWt), harvest weight (HrvWt), average daily gain (ADG), hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), dressing percent (DP), yield grade (YG), quality grade (QG), and Warner-Bratzler shear force (WBS) were set as random variables, while year was set as fixed variable. Overall means were calculated to report the total average for each trait after completion of 10 years of improved sire selection.

Results

Evaluation of the feedlot traits revealed that harvest weight and average daily gain exhibited an increase every year, whereas feedlot entrance weight has actually been decreasing over the 10 year period. Specifically, feedlot entrance weight decreased at a rate of 0.76kg per year, with a decade average of 253.48kg (Figure 3.1). Harvest weight increased at a rate of 7.72kg per year and averaged 556.02kg over the ten year period (Figure 3.2), and average daily gain exhibited an increase of 0.05kg per year, with a ten year average of 1.31kg (Figure 3.3).

In analyzing the carcass composition traits, positive rates of change were observed in all traits. Specifically, hot carcass weight realized a 5.64kg increase per year with a decade average of 338.32kg (Figure 3.4). Rib eye area also showed a positive trend, increasing at a rate of 0.28cm^2 yearly and averaging 33.54cm^2



Entrance weight (kg)
Average: 253.48
Slope: -0.755

Figure 3.1: Mean of feedlot entrance weight, kg, for steers participating in the ABBA carcass evaluation program for years 2004-2013

over the ten year span (Figure 3.5). Finally, as seen in Figure 3.6, yield grade increased at a rate of 0.7 units per year with a decade average of a 2.39 YG score.

Analyses of the carcass quality traits revealed that marbling score, quality grade, dressing percent, and Warner-Bratzler shear force showed an average increase over the ten year span of data collection. Specifically, marbling score increased at a rate of 0.86 scoring units per year, with a decade average of 370.70 (Figure 3.7). Quality grade also increased, ascending at a rate of 0.066 units per year and averaged a quality grade of 657.05 over the ten year period (Figure 3.8). Dressing percent also improved, rising at an average of 0.163 percent each year to a decade average dressing percent of 63.71 percent (Figure 3.9). Finally, an unfavorable increase was seen in Warner-Bratzler shear force scores, indicating a negative trend for tender beef. Warner-Bratzler shear force scores increased at a rate of 0.27kg per year, for a decade average of 7.86kg as can be seen in Figure 3.10.

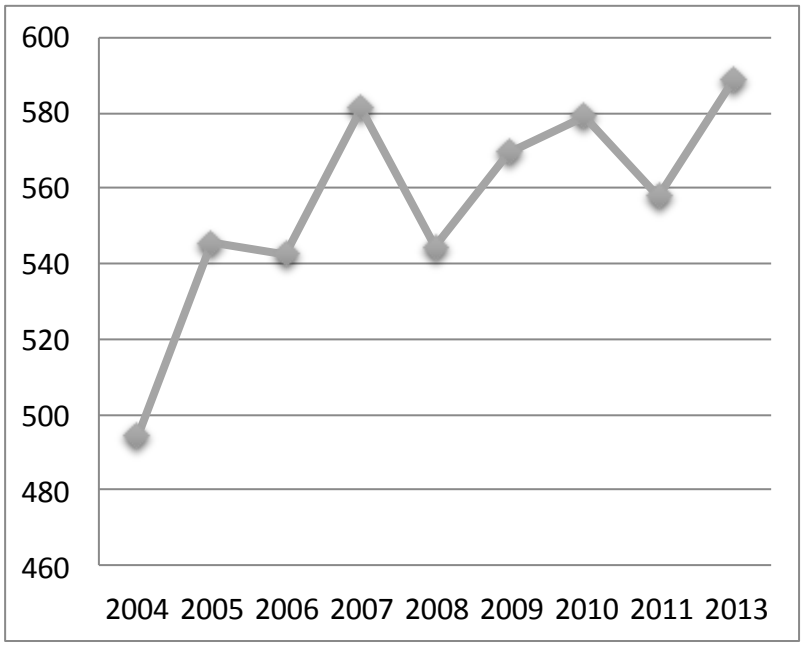


Figure 3.2: Mean of harvest weight, kg, for steers participating in the ABBA carcass evaluation program for years 2004-2013

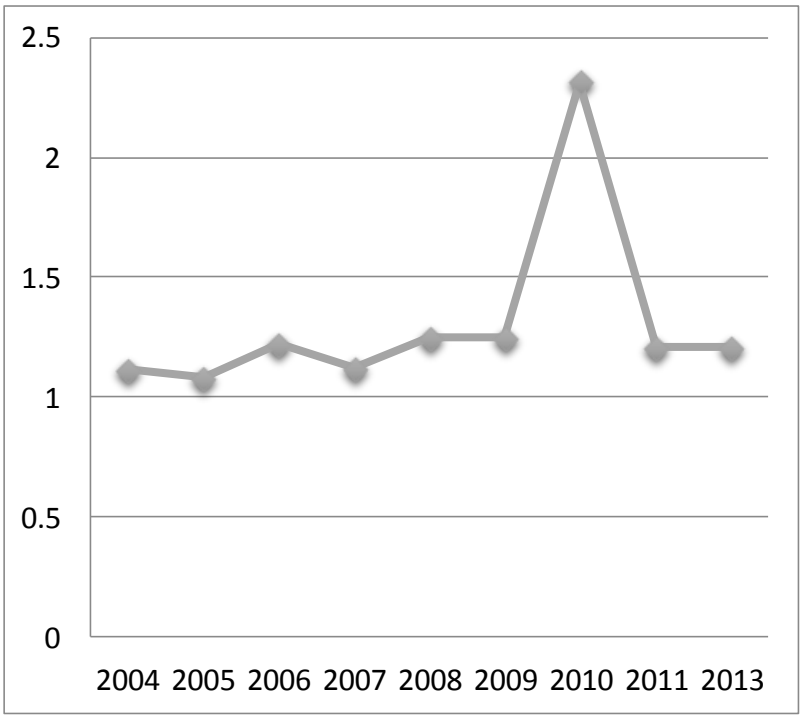
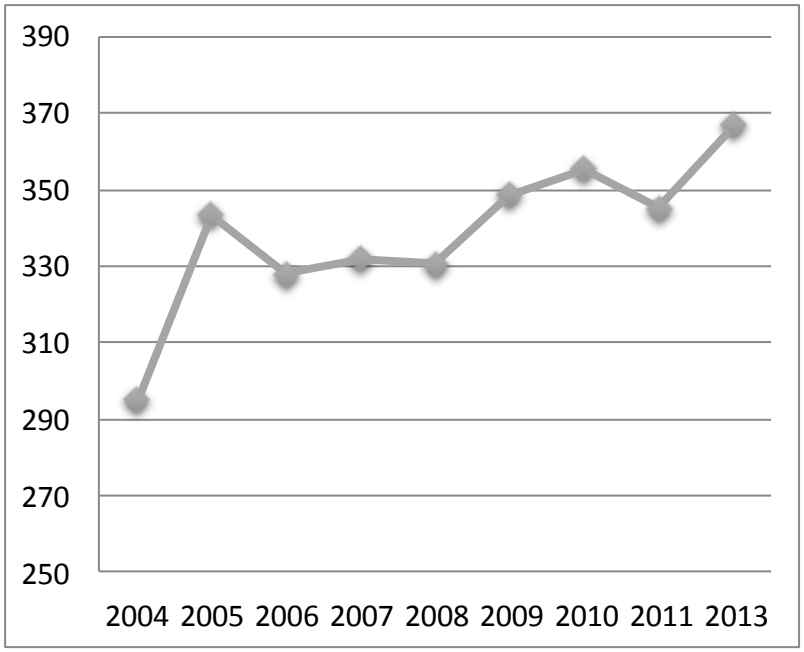
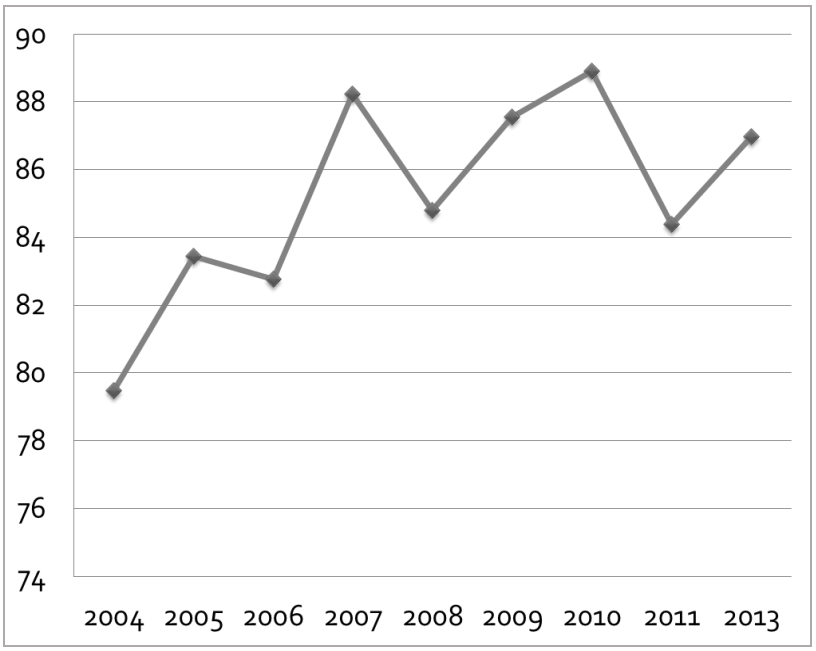


Figure 3.3: Mean of average daily gain, kg, for steers participating in the ABBA carcass evaluation program for years 2004-2013



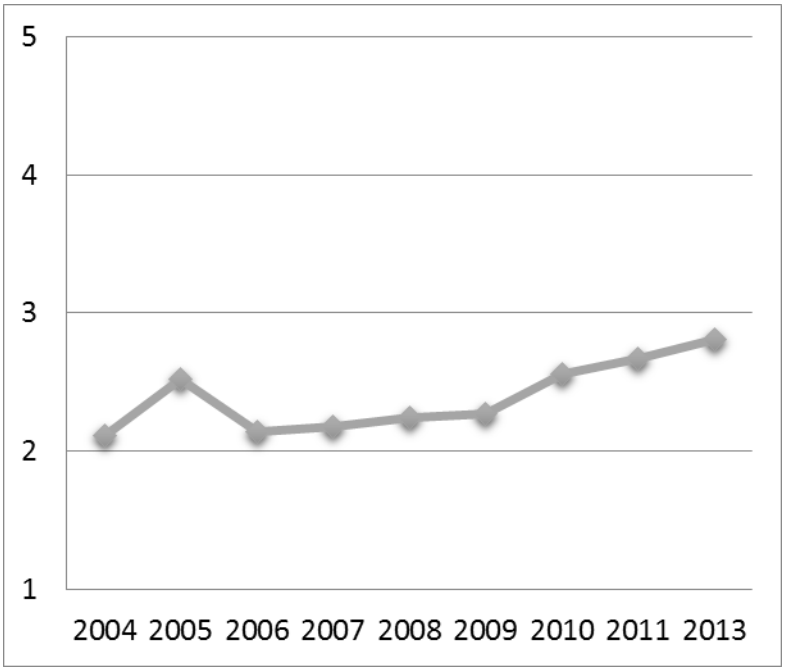
Hot carcass weight (kg)
Average: 338.32
Slope: 5.64

Figure 3.4: Mean of hot carcass weight, kg, for steers participating in the ABBA carcass evaluation program for years 2004-2013



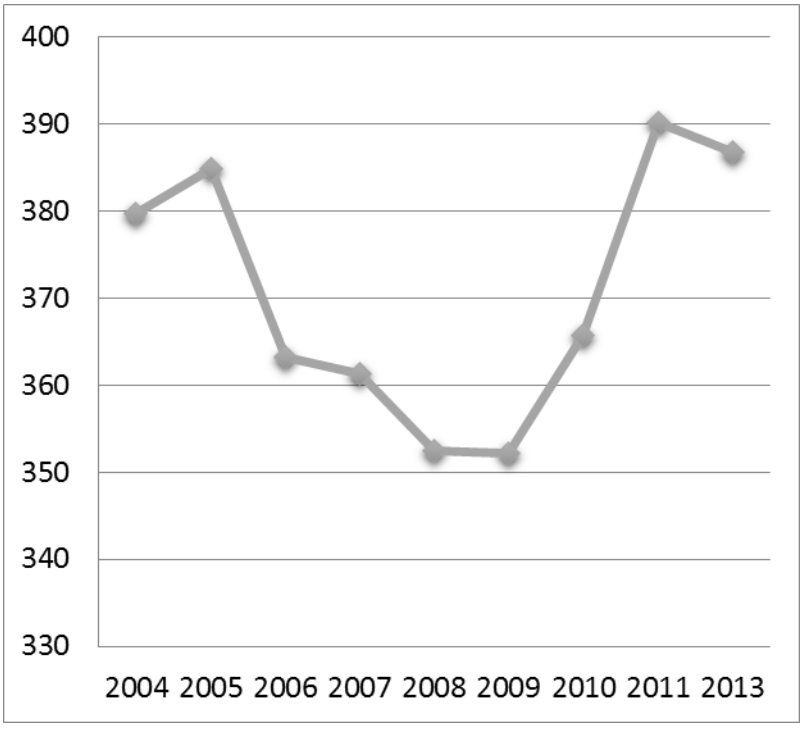
Rib eye area (cm^2)
Average: 85.17
Slope: 0.276

Figure 3.5**:** Mean of rib eye area, cm^2, for steers participating in the ABBA carcass evaluation program for years 2004-2013



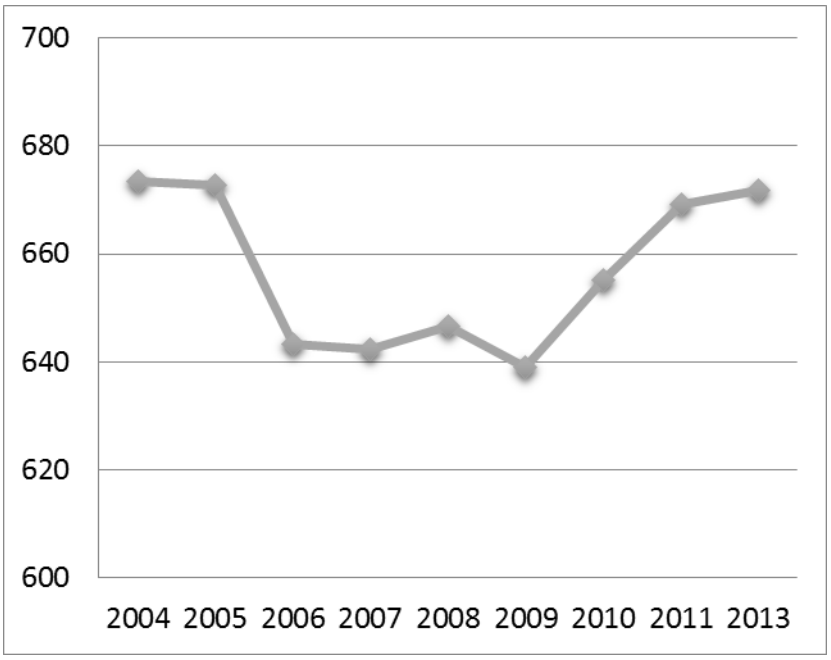
Yield grade (units)
Average: 2.39
Slope: 0.066

Figure 3.6: Mean of yield grade, units, for steers participating in the ABBA carcass evaluation program for years 2004-2013



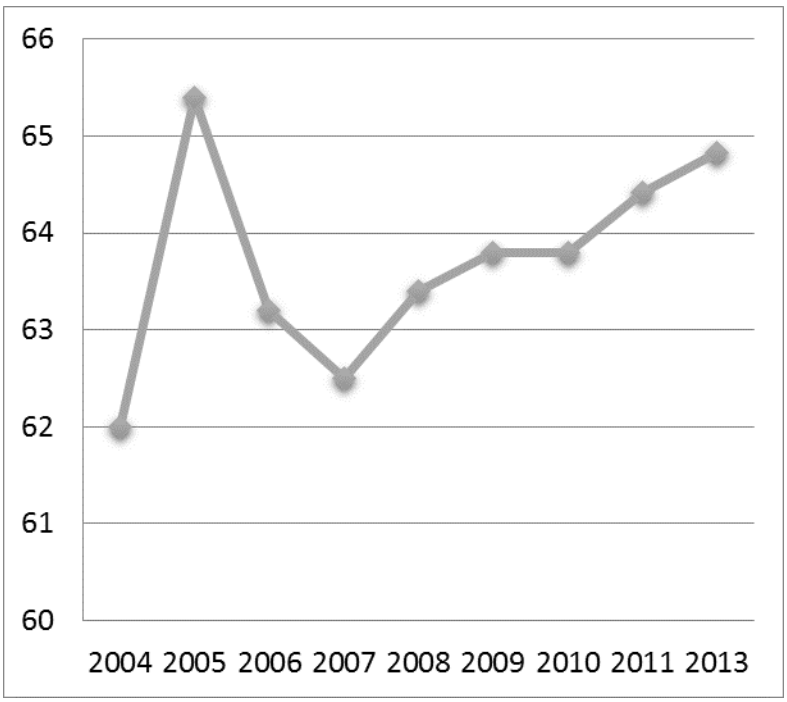
Marbling score (units)
Average: 370.70
Slope: 0.86

Figure 3.7: Mean of marbling score, units, for steers participating in the ABBA carcass evaluation program for years 2004-2013



Quality grade (units)
Average: 657.05
Slope: 0.066

Figure 3.8: Mean of quality grade, units, for steers participating in the ABBA carcass evaluation program for years 2004-2013



Dressing percent
Average: 63.71
Slope: 0.163

Figure 3.9: Mean of dressing percent, units, for steers participating in the ABBA carcass evaluation program for years 2004-2013

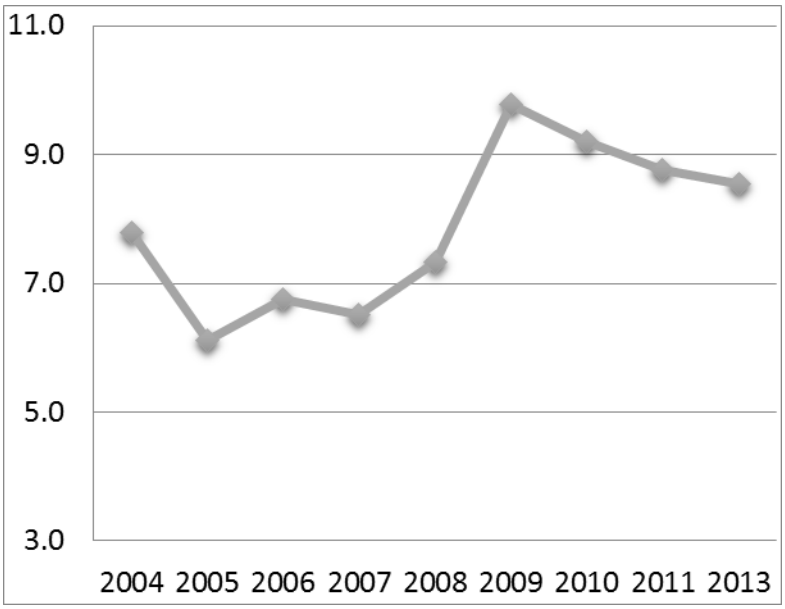


Figure 3.10: Mean of Warner-Bratzler shear force, kg, for steers participating in the ABBA carcass evaluation program for years 2004-2013

Discussion

A total of 595 steers were included in this trend study of the American Brahman Breeders Association carcass evaluation program. The study plotted data from years 2004-2013 in order to track improvement in performance and efficiency in the feedlot, as well as improvement in carcass quality and composition traits. Positive, favorable changes were seen in eight of the ten economically important traits reported. The increases in yield and quality measurements indicate that improvements have in fact been made in Brahman carcasses over this 10 year period.

The positive slopes of all feedlot traits with the exception of INWT indicates an increased level of performance seen in the feedlot. A decrease in INWT suggests cattle entered the carcass evaluation program at lighter weights in recent years, but an increase in ADG and harvest weight indicate favorable improvement in feedlot efficiency for Brahman cattle.

Carcass quality and composition traits saw favorable increases except for shear force scores. Marbling, quality grade, yield grade, rib eye area, and hot carcass weights all showed positive improvement. An increase in quality grade is promising, as Brahman cattle have also been reported to have lower quality grades (Wheeler *et al.,* 2001). While the slope was positive like the rest of the favorable upturns, the increase in shear force is highly unfavorable. An increase in Warner-Bratzler shear force score is an implication of less tender meat, which Brahman cattle have previously been reported to have as compared to their *Bos taurus* counterparts (DeRouen *et al.,* 2014). However, shear force scores in the carcass evaluation program have been on a downward trend since 2009 according to Figure 3.10. In years to come with proper genetic selection, the average yearly change could become negative, as would be favorable for more tender beef.

This study detailed the improvements and retrogressions made in the feedlot performance of the Brahman breed in the first 10 years of the carcass evaluation program. The ABBA carcass evaluation program and Brahman producers have made improvements in production, efficiency, and carcass traits in a relatively short period of time. After ten years of evaluation, Brahman cattle are entering the feedlot lighter, but gaining more and harvesting heavier than they were in the beginning of the program in 2004. Also, not only are Brahman steers harvesting heavier than in years past, they are yielding improved carcasses on many fronts. This is apparent in the rising marbling scores, dressing percentages, and quality grade scores, but additional improvement is still needed in relation to tenderness. Through this program, participating Brahman breeders can visualize the changes in the breed achieved as a direct result of refined genetic selection practices. Continued priority for breed improvement will likely make the Brahman breed competitive in performance, quality, productivity, and profitability in comparison with other beef cattle breeds.

CHAPTER IV
AN SNP ASSOCIATION STUDY EVALUATING BRAHMAN AND BRAHMAN-INFLUENCED STEERS FOR GROWTH AND CARCASS TRAITS

Introduction

Multiple tools have been developed to improve accuracy of animal selection and rate of improvement in economically important traits in beef cattle. Identification and utilization of molecular markers has been reported to increase the rate of genetic improvement as compared to other currently utilized selection tools (Davis et al., 1998). The candidate gene approach evaluates single nucleotide polymorphisms (SNPs) located on genes of known physiological function, and analyzes potential associations with economically important traits. This may be especially useful for Bos indicus cattle, who are known to exhibit less desirable growth, performance, and carcass characteristics when compared to Bos taurus cattle (Wheeler et al., 2001). Economically important traits have been reported to vary in heritability (www.uaex.edu/publications/pdf/mp184/chapter4.pdf). This makes improving traits such as fertility and carcass traits, which are lowly heritable and difficult to measure, a challenge within the Brahman breed. The use of molecular markers may increase the rate of improvement within these problematic traits.

The current study evaluated SNP's located on six candidate to evaluate potential associations with growth traits, feedlot performance, and carcass traits. The candidate genes included Adiponectin (ADIPOQ), Thyroglobulin (TG), Calpain-III (CAPN3), Calpastatin (CAST), Insulin like Growth Factor (IGF1), and Growth Hormone (GH1). Adiponectin was selected because of previous reports indicating its proximity to a QTL on BTA1 associated with marbling, ribeye area, and backfat thickness in Angus cattle (Morsci et al., 2006). Furthermore, a separate study identified two SNP significantly associated with increased ribeye area and backfat thickness in Hanwoo cattle (Shin and Chung, 2013).

The Calpain (CAPN3) and Calpastatin (CAST) genes were selected because of previously reported associations with meat tenderness. Calpain is a skeletal muscle specific calcium-activated protease previously

associated with myofibrillar protein breakdown (Wheeler and Koohmaraie, 1994). Barendse and associates reported (2008) a higher frequency of the CAPN3 SNP in zebu cattle than taurine cattle, and attributed the variation in tenderness of Bos indicus cattle to the higher frequency of that allele. Calpastatin is a protein that inhibits protein degradation postmortem and has been associated with the CAST gene and meat tenderness (Shenkel et al., 2006; Koohmaraie et al., 2002). Jointly, CAPN3 and CAST interact together to contribute to meat tenderness. Calpain accelerates protein breakdown, calpastatin inhibits calpain activity, thus playing a regulatory role in postmortem proteolysis (Koohmaraie et al., 2002; Schenkel et al., 2006). This calpain-calpastatin complex has been reported to play a role in Brahmans ability to thrive in tropical conditions, but results in tougher meat than taurine cattle (Schenkel et al., 2006). These independent associations along with these joint interactions make CAPN3 and CAST likely candidate genes for carcass quality and composition traits.

The Thyroglobulin (TG) gene which is located on BTA14 was selected as it has been previously reported influence on marbling measurements in beef cattle (Casas et al., 2005). A higher frequency of the favorable T allele reportedly showed higher marbling scores (Barendse et al., 1999). Brahman cattle have exhibited lower frequencies of the previously reported favorable T allele than Bos taurus cattle and Wagyu cattle (Casas et al., 2005; van Enennaam et al., 2007).

Insulin like Growth Factor (IGF1) which is located on BTA 5 was evaluated in the current study as previous research has indicated the gene's influence on growth traits and carcass traits in beef cattle (Machado et al., 2003; Pereira et al., 2005). IGF1 is released from the liver upon stimulation by growth hormone and is involved in mediating bodily growth and development. IGF1 plays a role in stimulating protein metabolism, cellular proliferation, and differentiation (Bauman, 1992).

The Growth Hormone gene (GH1) selected as a candidate gene in the current study as it has been associated with growth regulation, the mammalian growth curve, carcass quality, and composition (Mullen et

al., 2010; Pereira et al., 2005). Located on BTA19, GH1 has been significantly associated with the level of growth hormone found in plasma, which stimulates IGF1 production and release upon reaching the liver (Mullen et al., 2010).

The objective of this study was to evaluate SNP located on six candidate genes and their potential association with growth, carcass composition, and carcass quality traits in a population of Brahman and Brahman-influenced steers.

Experimental Animals

The population of animals utilized herein included forty-two Brahman and Brahman influenced steers born between 2009-2014, at the LSU AgCenter Central Research Station located in Baton Rouge, Louisiana. Specifically, 31 were purebred Brahman and 11 were F1 Brahman crosses. Steers were evaluated for growth and carcass traits through the American Brahman Breeders Association (ABBA) Carcass Evaluation Project in Gonzales, Texas.

Growth and Carcass Characteristics

Data collected at the Central Research Station included sire and dam, sex, birth weight (BW), weaning weight (WW), and hip height (HH). All bull calves were weighed and castrated within 24 hours of birth. Spring-born calves were weaned at approximately 205 days, when weaning weights and hip heights were recorded. Steers that met criteria for nomination to the ABBA National Carcass Evaluation Program completed a backgrounding program 45 to 60 days prior to being shipped (http://www.brahman.org/wp-content/uploads/2014/10/ABBA-Carcass-Evaluation-Program-Guidelines.pdf). Steers were delivered to Graham Land and Cattle Company in Gonzales, Texas, for evaluation of feedlot performance.

Feedlot performance traits measured included feedyard entrance weight (INWT), harvest weight (HRVWT), and average daily gain (ADG). Steers were processed individually upon arrival to the feedyard and were sorted into an appropriate pen based upon weight, frame size, and condition. When individual pens reached an average

weight and body condition deemed acceptable (one centimeter of backfat and 544 kilograms body weight) animals were sent to a commercial packing plant for the collection of carcass quality and composition traits. Carcass traits collected included hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), yield grade (YG), quality grade (QG), dressing percent (DP), and Warner-Bratzler shear force score (WBS).

DNA Extraction

Twenty milliliters of blood was collected from each steer via jugular venipuncture. After collection, blood was transferred to two 15ml tubes and centrifuged at 4000rpm for 20 minutes at 4 degrees Celsius. White blood cell buffy coats were then extracted and deposited into 1.5 milliliter micro centrifuge tubes. DNA was then extracted from buffy coats using a Saturated Salt Procedure previously described by Miller and associates (1988) (Appendix A). Purified DNA were diluted into 25ng/µl working solutions in preparation for genotyping.

SNP and Genotyping

Previously described SNP's were selected equidistantly across the TG, ADIPOQ, CAST, CAPN3, IGF-1, and GH1 genes for genotyping from the dbSNP website (http://www.ncbi.nlm.nih.gov/projects/SNP/). Equidistant spacing was conducted to account for possible linkage between selected SNP's and a potential causative SNP accounting for a large degree of variation in the trait. Genotyping was performed by Neogen, Inc. in Lincoln, Nebraska using the Sequenom genotyping platform. Single nucleotide polymorphisms, allele substitutions, and upstream and downstream sequences for genotyped SNP's are reported in tables 4.1, 4.2, 4.3, 4.4, 4.5, and 4.6.

Statistical Analysis

The mixed model procedure of SAS (version 9.4, SAS Institute, Cary, NC) was used to evaluate potential SNP associations from candidate genes ADIPOQ, CAPN3, CAST, TG, IGF1, and GH1 with growth traits, feedlot performance, and carcass traits. Models were fitted individually for each trait. Dependent variables in the model included birth weight (BW), weaning weight (WW), hip height (HH), entrance weight

Table 4.1: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for TG.

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs110501231	C/T	ACGATTGGGATGTTTCTGTACCAAGG	CACTTTGGGTGGAAGGGGAGAATGA
rs135059985	C/T	GTCTTGAGCACTGGAACTTCATTTGA	CATCTAAGATGGCAGTCCTGCACTTG
rs136379742	C/T	CAGGCCCCCAGGGTCTTCTCGCTGTG	CCCCATCAGAACAGGAGCCCTTGGC
rs378567477	C/T	TGAGGAGCTCCTGTCAAGCTGAAAA	CTCAGCCCCAGCATCACCTCCCCCAG
rs383724494	C/T	AAGTGGACGGTGGAGGGCTCACCAC	TCACATCCAGACCACAGAGGCGGCA
rs136849694	A/G	CTGGCCACAGCGGTGGGGAGGCGGG	GGGGCCCCCACCGGAAGTGGACGGT
rs379996188	C/T	CTGACCCAGAAGGCCTTCCTGGGTGC	GGCACAAAGGTACAGGTGAGGGGG
rs110999400	C/G	GCTATATTCCCACGTCTAATATCAAG	TGGAAAGACGGAAGAGTGAGGGGC
rs133473042	C/G	CCTTCTGTGACTCACTTCACTCAGTA	GACAATCTCTGGGCCCATCCATGTTG
rs110191002	C/T	CTTTTAATCTTCTCTCCATTTGCTGCA	AGTGGGTTCTTGTTGGTTATCCATTC
rs109182502	C/T	GGATGTTTCTGTCCAGCCATTGCTCC	GTGGCTCTGTTTCAGGGACCGGCTG
rs382252585	A/G	AAAGTAATTTCCAAATTACAACTTGT	AAAGTGCCTAGGTACCTGGATGTTTC
rs380627374	A/G	TTCATACACACACGCAGTAGGGGAA	TGTCGCCTTTGAAAAGTAATTTCCAA
rs132813094	A/C	TAAAAGGTAATACCCTGACTCCTGGC	AAGGCAACGGCCGCCTTCTGATTTCA
rs133980693	A/G	CCCTTCTCCTGACATCTCTGGCAAAC	CTCCTTCCCACCTGGCTCGGTTACAA
rs377997897	C/G	ACTTAAATACAATTTTCTGAGTCAAG	AGCAATGACTGTGAGATATTGTTAGC
rs109830314	C/T	CGTCTCCTGCACTGCAGGTGGATTTT	TGACCACTGAACTAGCAGGGAAACC
rs29021775	A/G	CAGTGGCTATGCCTGCTTTCCTCTCA	CAAGAGTCAGGTTATATTTTAGTAAG
rs109188488	C/G	GTGGGTTCTGGTTCTGGTCAGTCTCA	GGTGGCTTTTCCATGCCACAGACTTA
rs110946911	G/T	CACAGAGCTTTGTCTTTCACGAGCTC	CCTAGGCTGTAATTCATCCCTGCAGT
rs110553649	A/C	ACGAGTCAGCAACTCACATACATAG	CCTTGTTAGTGTCCTTTGAATATCAG
rs110187386	C/G	ACTCTGCAAACTAAAGCAAGAGATA	ACTTCAAAAAAAAAAAATCTTCTATAC
rs378900777	C/T	CTGGGTTTATTGTTACTGTTTGGTCA	GTCCAACTCTTTTGTGATGCCATAGA
rs381723399	C/T	TTTCTTCCCAACCCAGGGATCAAACT	GAATCTCCTGCATTGCAGGCAGATTC
rs384062524	C/G	CTGCGTGGGATGAACAGGAGAGGTC	TGTCTGAAGCAGGGATTACCACAGA
rs110616947	A/C	AGAATTAACTAATCCATCCATTGATT	ATCCATCCATTCACTTACACAGTTGCT
rs109068240	C/T	TCTCCAACACTGCAGCTCAAAAGCAT	GATTCTTCAACTCAGCCTTCTTTATGG
rs379467464	C/T	AGTGAATGGCTGGATGGCTGACTGA	GGCTGCGTGGGATGAACAGGAGAG
rs386026054	C/G	ACTCTGCAAACTAAAGCAAGAGATA	ACTTCAAAAAAAAAAAATCTTCTATAC
rs134743669	A/G	GGTAGACTACAACCGAGGGGGTCGC	AAGAGTCAGACACGAGTCAGCAACT

Table 4.2: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for ADIPOQ.

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs380209068	A/G	AAAACACCCTAACAATTCCCAAACT	TTGATTACTAAATCCAAAACTACCTCT
rs209727017	C/T	ACCAATTTGAAACACTCTACTGAGA	AGATACTTTGTTGTTAAGAAAGGGA
rs380391978	A/C	AAATAATGCAAATAGAAGGAAATA	AATTTCCCAAATTTTATTTGGGGCAG
rs208856619	C/T	CTGGTCTCTCCTGGTTGCCAGCTCCT	TCTTAGGATGGGGGTACCCAGGAAA
rs383535987	A/G	CATTGCTCCTCTGTGCCTGTGCACAG	TGTCCTTCTCTTTCCTCTCCACTTGGA
rs133746968	A/G	AGCTTCATGCACACTGGCTGTGGGG	CCAAAGGAGGCCATGTCTGTCAAGC
rs385926794	C/T	GAAGGAGTGAAAGGATCAGGGACA	AGCCAGGAAGGGGCTGGAGAATTCC
rs385383313	A/G	CCCTCCCTTTAGGGAAGGAATCTGC	CAACCTTTCAAGGGTTTCTGAATGCA
rs210865525	C/T	ATGTTGTTAATGCAGCAATGGACTC	GACTGCTTAGAAAAACCCCAATCTGT
rs208093103	A/G	CGGTACAAGAGACACAGGAGACGC	GGTTTGATGCCTGGGTCAGGAAGAT
rs378178622	C/T	CAGTAGCCTGGGTGACCTGGAAGGC	ACTGTGTATAAGCCCCTGGAAAAGA
rs209050698	A/G	TTCCAAGTACACAACACGTATTATT	ACTAGAGGCCCATGACCCAGTTTTGA
rs382192949	A/G	CTGATGCTCAGCTTTAGAGTACTGC	TTAGCAACTCATGTTTTAAAAAATAA
rs208699764	C/G	AAATACATGTGAGCCTTTCCTCCAG	GTGTGTCATGGTTACCATTCAGTCCC
rs211230641	A/T	TTTAGTCCCCAAATCGCATGGCTAC	GTGCTTACCTGGCTGTCAGACAGGA
rs378724414	A/T	CGCCAATATTTTATTTTTATTGTGGC	TCTCTGATTTATTTTGGGTTTGTATTA
rs382701614	C/T	GCGACTTAGCAGCAGCAGCAGCACA	GCTAGTAAAGTAATGCTCAAAATTCT
rs386011953	A/G	GTGAAAGTGCTGCACTCAATATGCC	GCAAATTTGGAAAACTCAGCAGTGT
rs379059851	C/T	CATGTGAATGCAGAGTTCCAAAGAA	AGCAAGAAGAGATAAGAAAGCCTTC
rs381854487	A/G	GGCTTTGGCGTAGTCAATAAAGCAG	AATAGATGTTTTTCTGGAACTCTCTT
rs383391069	C/T	TTTTAATTTCATGGCTGCAGTCACCA	CTGCAGTGATTTTGGAGCCCAGAAA
rs380790166	C/T	TTTCAGTCCAAGGGACTCTCAAGAG	CTTCTACCTCACCACAGTTCAAAAGC
rs382644882	C/G	TTTGCCAAGACAGAGTTCAAGGTGA	GAACACTGCCACTTTAAATCTAAGCC
rs381911082	G/T	GGTGGTACAAGTGGTATAGAACCAC	TTATGCCAATACAGAAGACACAAGA
rs209420330	C/T	GGGAACTGCAGTATAGCAAGAAATA	AATACATCCTTTCCTCTCTGGCCTGAA
rs210607551	C/T	CCCTGGCAGCTCCTTTGGCTTGCCAC	CCAGGGAACCTGGTGCAACCCAGTT
rs384076273	C/T	AGAACTTGAATCAGTCGTCCTTACC	TCAGGTGTGGAATCAGAGCCACAGA
rs209743114	C/G	CTATTAATAGACTATTTCACAATACT	TTGTGAGAACAGGTTCACTTAAAGTA
rs210601764	C/T	GTGCAGAGATGCTGAACTTTCAATT	ATTTTAAAACTGTGTGTGCTCCCTATT
rs210258853	A/G	GGAAATACAGAGAGAGGAGGGAAG	AGGAAGGAAAAGAGAAAGGAAGAG

Table 4.3: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for CAST.

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs137780582	G/T	TAAGAAAATAAAAAAAAAAAAGAAC	CTTAACCCCACGATCAGAAAATAACC
rs137777861	G/T	CTGGTGAATGAATAAACTAATATATG	TGAATTGAGCCATCACGTAATACTCA
rs137726884	A/G	AAACTTACCATTTAAATGTTCCCCTG	AAGTTGCAAGTCTTTGATAGACTCCA
rs137722600	C/T	CCAAGCAGAAGACGTGGGTTCTATCT	GGGGTTGGAAAGATCCCCTGGAGAA
rs137711215	A/G	AAAATGTTAGAGAAAAGCAAAGGGA	TTCAGGGAAACATGAGGATTTCAGA
rs137662301	C/T	ATGGGGTCACAAAGAGTCAGACATG	CTCAGCAGTCAGACAAACAGCAAGG
rs137601357	C/T	AGAACTCAGGCTGGTGAAAAAGCCC	GGTCCCCAAGGTCAGTCATTTCCTGG
rs137561617	A/T	ATTGAATTTAACTTTTACATGCTGAT	TTCAGTATCTAAAGGATATTTATTGC
rs137374423	G/C	ATCATTTTCCTTTCTGTTCCTCAGACT	TATAATTTCAGTTGTCCTATTTTTGAT
rs137330201	A/G	GCTCATCTGCTCACCCTTTATCATTTT	TTGATTCTTTGCTAGCAGTATTGGCA
rs137265200	C/T	CAAAGAGTCAGACATGTCTCAGCAG	CAGACAAACAGCAAGGGTGTTAATG
rs137211570	A/C	CCAGGCCTCCCTGTCCATCACCAACT	CCGGAGTTTACTCAAACTCATGTCCA
rs137151719	G/T	AGTTCAAGTGTAAGTGTATTCTTCCA	AAGGAAAAGCATTTCCTTATCTCTCC
rs137140434	G/T	TTTCAGTTATTATATGTCTCCACTCTA	AATTTTTTTTTGGTTTCTTTTTAGATG
rs137104571	G/C	AGTGGTTCTGCTTCTGGGCCAAAGAG	GCTGAAAAGTGAATTCTCTCAGTCGT
rs136982429	C/T	CAGGCAAGAATACTGGAGTGGGTTG	CATTTCCTCCTCCAGGAGATCTTCCCA
rs136882857	C/T	CAGATCTCCTGCCTGGGAAGGGCCTT	ATTCATTTCATTCATTCAAACTCTTGG
rs136875549	C/T	CATAACTTCCACCTTTTGTGGCTTTTT	CCTAAGCGTTTGGGGTGCTCCTGTGT
rs136882857	C/T	CTCCCGAACTACAGGCGGATTCTTTA	GAACTGAGCTAGGAGGGAAGCCCA
rs110496242	A/G	CCTTTGGTAGATAAACGAAAGAGAA	GGAACCTACTGTAGGAAATCATCAA
rs134030456	C/T	CAGTGGAGTTACTCTGATCCCCCGC	GCACACTTTTCCGTATGCTGTTATG
rs109702795	G/T	CATCAGGAAATAYGGTCCAGCACAC	GGATGTTTTCAACAGTGTAACTAAT
rs110136749	A/G	AAATTAGAAATCTGTCTTTGCAAAA	GGTTCTAGGTGCTTCTATTTATAAA
rs110374623	C/T	AGTCTGAATTTTGCTTGAAAAGATA	TTGTATTGACAGAAAAATTTGCGGT
rs133120980	A/C	GAAGGAGCACCTAGGCTGAGGATAG	CCCGGGACTGGGAGCTGAGGGAGCT
rs133891017	A/T	ATCAAGCAGAAACTAAAGATCAGAG	GTTTAAGTAGCTTGCCCAAGATTAT
rs137371179	C/T	CTCACTCAAACATATCAGAAAAAGA	AGTCTCTTCTCTCATATCCTGGAAT
rs109020860	A/G	CTGTCGTCCTGAGTGTGACTGCCAG	GCTTAAGAGCAAGTTAGCTCCTTTC
rs110386026	C/T	AGCCAGGCCTTTGAAATAAAGTCAG	TTGAAAATGTGCTTTCTCTGCTCAG
rs136873074	C/T	TCCCGAACTACAGGCGGATTCTTTA	GAACTGAGCTAGGAGGGAAGCCCA

Table 4.4: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for CAPN3

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs109372443	A/G	TTATCCAAATGTGCTTTTATATGTCA	TCCTCAGCATGGTGGAATCTTCAGC
rs135512997	A/G	TCAGGGTGCCATGGGATCAGAAGGCA	GGAGAGTTAACCTAGGCCAGAGAGA
rs43624105	C/G	GACTCCCACCTGCCTTACACATTTGT	TCATTTATCCATTGGTTCAAAACTC
rs136324366	A/C	GTCTGGTCTGCTTCATCCTGCTGGGG	TGGTTTGGTTGGGATGGTCAGGCTG
rs43624107	A/C	ACACAACTTGGGGCCCAAGCATGGGT	TGGGCCACACAGGCCATGGAGTGTA
rs43624108	G/T	TTTATAGTCCATTCTGCCATTGGTCG	GGCCAAGGAAGGGGAGCTTCTGGCA
rs109122904	A/G	TGCAGCGTTACCAGGGTCCTGGGTCC	CCTGGGGCACATCAGGGCACCTCCT
rs136966673	A/G	GACATACAGATGGCTAACAAACACAT	AAAAGATGCTCAACATCACTCATCA
rs134085397	A/G	GCTATATTCTCCAGTCTCAGATCTTG	GGTCCACTTTCTGCCAACTCCTCCA
rs137379223	A/G	TGCTCAGTTTATGTTTATTTTTAGTG	TAAAGATAGCAATTGCCCCAACATT
rs110247569	C/G	ACTGGGAAGACTTACCCAGTGAACAG	AGCACAGGGCTTTCCTCTGGGGCAG
rs109806627	C/G	CCTCCCCTCTGCAGTCTCAAAGATGC	GTGACATCCCACACGGCACAGCAAA
rs109337751	C/T	GGGTGGTGTGTGTGGTGTGATCTATG	ACGACTTTCCATCTAGTAGGTGAGA
rs134606436	A/C	GAACAGCCACGTCATCAGTGCATGCG	AGTCACGTGATCAGTGCATGAGAGC
rs41644730	C/T	CCTTGGGTCTACAGGTTCAGAAGCCT	GTCCCCCCATCTGCCACCAATTCCA
rs133798263	C/T	AGGACGCCTGCGGCCTTCGTAGGTGA	GTAAATTCCCTGCTTTGGAATTTTA
rs110452450	A/G	TGCTAGGTTGATGGGTTTTTGTATCA	TTTAAATATTTCAATCCGATCTTTC
rs135091523	G/T	TTCTCAACATTAAATATGATGATAAT	GTAGGTCTCTAAAAAAAGGTACATT
rs110822150	G/T	CCTCCTGATGGACAGGCTGCCAGAAT	GAGTTTCTCCCCGGGCCAGCTCCTT
rs109050259	A/G	TAAGTCAGATGGATTTAGAAGCAAAC	GACCTGGTCGGAACCCTGACTCTGT

Table 4.5: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for IGF-1.

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs137605212	A/G	CCACTCCCCTGGCAAGGACCCAGGAG	AAGATGACCCTCCTTCTGCTTTTTC
rs137250028	C/T	GGACAGAGCACATGACTAGCCAATGA	GCTATAATGGAATTGATTAGTTAGT
rs136493168	A/G	AACCACTTCCTGCTCCAAGTACAGGA	AAAGCAACAACTTATGGCTAGCTA
rs135968955	G/T	AGATAAAGGAGTCTAAAATGTTCTTT	GTCACTATTTGAATCCAAGATTCTC
rs135711837	G/T	GCGTACTTTTGATGGATTAAATATTA	AAAATATTAAGGAAATTCAAATCTA
rs135230510	A/G	TGAAACACTAGGCTCGCATTAAGGTG	GGAATCTCGGAGGCTGAGGACGGC
rs134494935	C/T	TTCCATCTTTGATTCTGTGTTAAGAA	CCCAGCCACTAAGCACCCCATTCTA
rs133980322	G/T	GCATTATTACTGTATCCATTTACAGA	GAGGAAATGGAGATTTAGCAAGG
rs133253110	C/T	GGCTTAGAGAATTCCATGGACCATAC	CATGGGGTTGCAAAGAGTCGGACA
rs132951819	G/T	CTTTGCAATAATATATTACCAACAAT	TCCCTTTGTTGAATGCTTTCTATTA
rs132665612	A/G	CAGTGAGTCAAGTGGACTGGAATAAA	TAGGGGAGAATTATTCCTGTCTGA
rs110959643	A/G	TCCCACACAAGATGGAGAGCAGACCC	TCCCAGTATTTGGGGAGGCCCATC
rs110266103	A/G	AGCAGTGAAACAATGCAAAGGTGATC	TTAAGTTTTTCCACATTGCTACTTG
rs109327701	A/G	AAGAATCGCAGTGTACTGGGTGAGAT	TGAACACCCAGCCATGCCTTAAACT
rs109227434	C/T	TCCATTTYCCTTTGGCCTGTCAAGCC	GTAGTRGTTGTGTGTACCCATAAGA
rs109199979	C/T	CAGCCTTTCTAGGACCTCAGCTAGAC	ACAGGTGAAAGAAGAAAAATCTGA
rs109074329	C/T	TAAGAGGAAGAAAGGRGGAGCATACC	GCCCAGCTAGCCCTGTTGACCAACT
rs109022910	A/G	TGCGAGCCTAGTGTTTCAGCGGGGCC	TGGCACGTTTTGCAGATTTTGGATG
rs43434843	A/T	AAACAATAAAGAACTTGCTTAGGAAT	AAAAAGTTTGAAATGAGTGGCCCCA
rs43434842	A/G	ATATGTGGGGGGCATATGTAAACTCA	ATGCCTATCAGAGCCACACAAGTCA

Table 4.6: Single nucleotide polymorphisms ID, allele substitution, forward and reverse primer sequences utilized for amplification and visualization of genotypes for GH1.

SNP ID	Allele Substitution	Upstream Sequence	Downstream Sequence
rs133438805	C/T	TCCATGCTGGGGGCCATGCCCGCCCT	TCCTGGCTTAGCCAGKAGAATGCAC
rs134389836	C/T	ACAGATCCCTGCTCTCTCCCTCTTTC	AGCAGTCCAGCCTTGACCCAGGGGA
rs133403174	A/G	CAGGGGAAACCTTTTCCCYTTTTGAA	CCTCCTTCCTCGCCCTTCTCCAAGC
rs137651874	C/T	CCTTGACCCAGGGGAAACCTTTTCCC	TTTTGAARCCTCCTTCCTCGCCCTT
rs137252133	A/G	CTTCCTCGCCCTTCTCCAAGCCTGTA	GGGAGGGTGGAAAATGGAGCGGGC
rs136132855	C/T	ACATGCGCAGTGACGACGCGCTGCT	AAGAACTACGGTCTGCTCTCCTGCT
rs109275907	G/T	TTAGCCAGKAGAATGCACGTGGGCT	GGGGAGACAGATCCCTGCTCTCTCC
rs135322669	G/-	GGGGTATGAGAAGCTGAAGGACCTG	CAGGAGCTGGAAGATGGCACGACA
rs134687399	A/G	ACTTCATGACCCTCAGGTACGTCTCC	TCTTATGCAGGTCCTTCCGGAAGCA

(INWT), harvest weight (HRVWT), days on feed (DOF), average daily gain (ADG), hot carcass weight (HCW), rib eye area (REA), marbling score (MARB), yield grade (YG), quality grade (QG), dressing percent (DP), and Warner-Bratzler shear force score (WBS). Independent effects in the model included breed and SNP genotype. Sire was fit as a random variable in the model. The LSMeans and the pre-planned pairwise comparisons function were used to determine individuals inheriting specific SNP genotypes were significantly different in their performance than other individuals inheriting a different genotype for a specific SNP. Any SNP with only one genotype was excluded from the analysis due to lack of marker effects.

Results

SNP ASSOCIATED WITH GROWTH AND FEEDLOT PERFORMANCE

Analyses revealed that when evaluating SNP associations with growth traits, a total of 28 SNP were found to be significantly associated (P<.05) with birth weight, weaning weight, and/or hip height. Furthermore, significant (P <0.05) SNP's were identified on all six candidate genes utilized in the current study. (Table 4.7).

Three SNP located on the TG (rs110553649, rs378900777) and ADIPOQ (rs210865525) genes were significantly associated (P< .05) with birth weight (Table 4.8). For marker rs210865525 on the ADIPOQ gene, heterozygote animals displayed a larger birth weight than those inheriting the major allele genotype. For marker rs110553649 on the TG gene, animals inheriting the minor allele genotype displayed a larger birth weight than those inheriting the heterozygous or the major allele genotypes. Animals inheriting the heterozygous genotype for marker rs378900777 on the TG gene displayed a larger birth weight than those inheriting the major allele genotype.

Fifteen SNP were found to be significantly associated (P< .05) with weaning weight (Table 4.8). Each candidate gene was represented, with six SNP from CAPN3, three from TG, two from IGF1, two from CAST, and one from each GH1 and ADIPOQ. (Table 4.8). When evaluating the six SNP associated with weaning weight located on the CAPN3 gene, a variety of genotypic effects were observed. Individuals inheriting the

heterozygous allele genotype for rs109122904, rs109337751, rs110822150, and rs109806627 had heavier weaning weights than those individuals inheriting the respective major allele genotypes. For marker rs109050259 on the CAPN3 gene, individuals inheriting the major allele genotype displayed heavier weaning weight than the heterozygous or minor allele genotypes. Animals inheriting the minor allele in genotypes from the final marker from the CAPN3 gene, rs109372443, displayed decreased weaning weights when compared

Table 4.7: Level of significance and frequency of animals from each genotype associated with farm growth traits

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Frequency[5]	Het Genotype Frequency[5]	Major Genotype Frequency[5]	SNP P-value	Breed P-value
BW[1]	ADIPOQ	rs210865525	C/T	0	1	40	0.0247	0.9135
BW	TG	rs110553649	A/C	2	20	19	0.0162	0.4128
BW	TG	rs378900777	T/C	0	2	39	0.0458	0.9770
WW[2]	IGF-1	rs109022910	A/G	4	9	26	0.0009	0.0001
WW	IGF-1	rs109227434	T/C	0	16	25	0.0238	0.0032
WW	CAPN3	rs109050259	G/A	2	23	16	0.0118	<0.0001
WW	CAPN3	rs109122904	A/G	0	5	36	0.0001	<0.0001
WW	CAPN3	rs109337751	T/C	0	14	27	0.0159	<0.0001
WW	CAPN3	rs109372443	G/A	11	13	16	0.0316	0.0224
WW	CAPN3	rs110822150	T/G	0	14	27	0.0159	<0.0001
WW	CAPN3	rs109806627	G/C	0	14	25	0.0192	<0.0001
WW	CAST	rs110496242	G/A	2	10	29	0.0060	0.1202
WW	CAST	rs137140434	G/T	0	5	13	0.0308	0.0838
WW	GH-1	rs137651874	T/C	0	6	29	0.0134	0.0742
WW	ADIPOQ	rs383535987	G/A	0	3	38	0.0287	0.0361
WW	TG	rs110553649	A/C	2	20	19	0.0083	<0.0001
WW	TG	rs378567477	T/C	8	16	9	0.0452	0.0228
WW	TG	rs386026054	G/C	3	24	12	0.0092	<0.0001
HH[3]	CAPN3	rs109337751	T/C	0	14	27	0.0476	0.5599
HH	CAPN3	rs110822150	T/G	0	14	27	0.0476	0.5599
HH	CAPN3	rs109372443	G/A	11	13	16	0.0028	0.9220
HH	CAPN3	rs109806627	G/C	0	14	25	0.0531	0.5522
HH	CAST	rs110496242	G/A	2	10	29	0.0362	0.7902
HH	CAST	rs134030456	C/T	0	15	26	0.0552	0.7172
HH	ADIPOQ	rs209050698	G/A	1	14	26	0.0217	0.0954
HH	ADIPOQ	rs210258853	A/G	1	14	26	0.0213	0.0954
HH	ADIPOQ	rs210607551	C/T	0	5	36	0.0037	0.4730
HH	ADIPOQ	rs210865525	C/T	0	1	40	0.0004	0.6798

[1]Birth weight
[2]Weaning weight
[3]Hip height
[4]Minor allele represented on the left
[5]Number of animals inheriting each gene

with individuals inheriting the major allele genotype. Three SNP (rs110553649, rs378567447, and rs386026054) from the TG gene showed a significant difference in weaning weights between the minor allele genotype and the major allele genotype. Markers rs110553649 and rs386026054 displayed larger weaning weights in the minor allele genotype than in both the heterozygous and the major allele genotypes. However, when evaluating marker rs378567477, the major homozygous genotype exhibited a greater weaning weight than in either the heterozygous or the minor allele genotypes. Two genotypes from candidate gene IGF1 showed significant differences in weaning weight. Marker rs109022910 on IGF1 showed individuals with the minor allele genotype had larger weaning weights than both the heterozygous and major allele genotypes. Individuals inheriting the heterozygous genotype from marker rs109227434 were heavier at weaning than individuals inheriting the major allele genotype. When evaluating the two SNP associated with weaning weight located on the CAST gene (rs110496242, rs137140434), individuals inheriting the major allele genotype for rs110496242 had significantly greater weaning weights, but were only significantly greater than the heterozygous genotype and were not significantly heavier than the minor allele genotype. For the marker rs137140434, animals inheriting the heterozygous genotype displayed heavier weaning weights than the major allele genotype. One SNP from the GH1 candidate gene and one SNP from the ADIPOQ candidate gene were significantly associated with weaning weight. When evaluating markers rs137651874 and rs383535987 analyses revealed that animals inheriting the heterozygous genotype exhibited greater weaning weights than those animals inheriting the major homozygous genotype. (Table 4.8)

Of the ten SNP found to be significantly associated with hip height, four were located on the CAPN3 gene, two on the CAST gene, and four on the ADIPOQ gene. Three markers from the CAPN3 gene (rs109337751, rs110822150, rs109806627) and one marker from the CAST gene (rs134030456) revealed a higher hip height for individuals inheriting the heterozygous genotype than the individuals inheriting the major allele genotype. Analyses of the CAPN3 gene marker rs109372443 and CAST gene marker rs110496242

revealed that individuals with the respective minor allele genotypes had larger hip heights than the heterozygous genotype individual. The hip heights of the minor allele genotype for CAPN3 marker (rs109372443) was also significantly different from the major allele genotype hip heights.

Table 4.8: Single nucleotide polymorphisms associated with farm growth traits and least square means estimate comparisons between reported genotypes. Differing superscripts indicate a difference of means at P<0.05 within rows.

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
BW[1]	ADIPOQ	rs210865525	C/T		50.50±6.44^{a}	36.12±2.26^{b}
BW	TG	rs110553649	A/C	48.31±5.04^{a}	37.44±2.36^{b}	33.33±2.26^{b}
BW	TG	rs378900777	T/C		45.56±5.06^{a}	35.93±2.36^{b}
WW[2]	IGF-1	rs109022910	A/G	290.58±16.07^{a}	221.08±11.36^{b}	217.88±7.48^{b}
WW	IGF-1	rs109227434	T/C		232.98±11.21^{a}	195.98±10.96^{b}
WW	CAPN3	rs109050259	G/A	147.98±31.52^{a}	219.29±6.73^{a}	239.76±7.94^{b}
WW	CAPN3	rs109122904	A/G		287.26±14.09^{a}	221.84±5.74^{b}
WW	CAPN3	rs109337751	T/C		240.46±8.35^{a}	213.48±6.62^{b}
WW	CAPN3	rs109372443	G/A	200.79±11.11^{a}	223.26±9.98^{ab}	235.18±9.20^{b}
WW	CAPN3	rs110822150	T/G		240.46±8.35^{a}	213.48±6.62^{b}
WW	CAPN3	rs109806627	G/C		240.46±8.59^{a}	213.33±6.92^{b}
WW	CAST	rs110496242	G/A	202.48±23.46^{ab}	180.92±11.48^{a}	227.97±6.70^{b}
WW	CAST	rs137140434	G/T		237.25±14.85^{a}	208.13±12.77^{b}
WW	GH-1	rs137651874	T/C		271.47±16.15^{a}	223.58±8.78^{b}
WW	ADIPOQ	rs383535987	G/A		274.54±20.19^{a}	224.38±6.42^{b}
WW	TG	rs110553649	A/C	291.48±22.62^{a}	231.95±7.43^{b}	210.88±10.06^{b}
WW	TG	rs378567477	T/C	198.82±17.43^{a}	216.32±10.16^{a}	256.61±16.50^{b}
WW	TG	rs386026054	G/C	282.21±19.08^{a}	228.67±6.84^{b}	198.34±17.33^{b}
HH[3]	CAPN3	rs109337751	T/C		114.98±2.64^{a}	109.61±1.77^{b}
HH	CAPN3	rs110822150	T/G		114.98±2.64^{a}	109.61±1.77^{b}
HH	CAPN3	rs109372443	G/A	105.97±2.01^{a}	113.08±1.91^{b}	113.02±1.80^{b}
HH	CAPN3	rs109806627	G/C		115.04±2.72^{a}	109.70±1.85^{b}
HH	CAST	rs110496242	G/A	116.87±3.96^{a}	107.68±2.56^{b}	112.38±1.73^{a}
HH	CAST	rs134030456	C/T		114.68±2.35^{a}	109.77±1.92^{b}
HH	ADIPOQ	rs209050698	G/A	116.84±5.84^{a}	113.68±2.29^{ab}	106.94±1.97^{b}
HH	ADIPOQ	rs210258853	A/G	116.84±5.84^{a}	113.68±2.29^{ab}	106.94±1.97^{b}
HH	ADIPOQ	rs210607551	C/T		104.48±2.73^{a}	112.41±1.62^{b}
HH	ADIPOQ	rs210865525	C/T		94.04±4.72^{a}	111.78±1.68^{b}

[1]Birth weight
[2]Weaning weight
[3]Hip height
[4]Minor allele represented on the left

Results indicated that two SNP located on the ADIPOQ gene (rs210607551 and rs210865525) showed significantly larger hip heights in the animals inheriting the major allele genotype than in the animals inheriting the heterozygous genotype. Two SNP located on the ADIPOQ gene, (rs209050698 and rs210258853), showed the hip heights of the animals with the heterozygous genotype were significantly larger than the homozygous animals, but were not significantly different from the minor allele genotype animals. Also, there was no difference between the major and minor allele genotype animals for these two markers (rs209050698 and rs210258853). (Table 4.8)

When evaluating feedlot performance traits, a total of 30 SNP were identified to be significantly associated (P<.05) with the feedlot performance traits that were previously described. Significant SNP's were located on all six candidate genes utilized in the current study as well. (Table 4.9).

Seventeen SNP were found to be significantly associated (P< .05) with feedlot entrance weight (INWT). Single nucleotide polymorphisms from 5 of the candidate genes utilized in the current study were significantly associated with feedlot entrance weight. Specifically, two SNP located on the IGF1gene, two located on the CAST gene, one from the CAPN3 gene, seven from the TG gene, and five located on the GH1 gene (Table 4.10). Analyses of SNP rs109022910 located on the IGF1 gene revealed animals inheriting the minor allele genotype had significantly heavier INWT than animals inheriting the heterozygous or major allele genotypes. Alternately, an SNP (rs109227434) located on the IGF1 gene showed animals inheriting the heterozygous genotype had significantly greater INWT than animals of the major allele genotype. The SNP rs110496242 located on the CAST gene showed individuals inheriting the major allele and minor allele genotypes had significantly heavier INWT than individuals with the heterozygous genotype, however a SNP (rs137265200) located on the CAST gene showed individuals inheriting the heterozygous genotype had significantly heavier INWT than those of the major allele genotype. The single significant SNP located on the CAPN3 gene

Table 4.9: Level of significance and frequency of animals from each genotype associated with feedlot traits

Traits	Gene	SNP ID	Allele[5]	Minor Genotype Frequency[6]	Het Genotype Frequency[6]	Major Genotype Frequency[6]	SNP P-value	Breed P-value
INWT[1]	IGF-1	rs109022910	A/G	4	9	26	0.0420	0.1068
INWT	IGF-1	rs109227434	T/C	0	16	25	0.0223	0.0070
INWT	CAPN3	rs109122904	A/G	0	5	36	0.0120	0.0643
INWT	CAST	rs110496242	G/A	2	10	29	0.0065	0.0651
INWT	CAST	rs137265200	C/T	0	5	28	0.0051	0.0438
INWT	GH-1	rs133403174	G/A	1	12	28	0.0139	0.0070
INWT	GH-1	rs133438805	G/C	1	12	28	0.0175	0.0070
INWT	GH-1	rs134389836	C/T	1	12	28	0.0158	0.0070
INWT	GH-1	rs136132855	T/C	1	12	28	0.0139	0.0070
INWT	GH-1	rs137252133	A/G	1	12	28	0.0139	0.0070
INWT	TG	rs378567477	T/C	8	16	9	0.0123	0.0168
INWT	TG	rs133980693	G/A	9	22	10	0.0058	0.0078
INWT	TG	rs110501231	C/T	9	22	10	0.0065	0.0078
INWT	TG	rs135059985	C/T	9	22	10	0.0064	0.0078
INWT	TG	rs110553649	A/C	2	20	19	0.0425	0.0737
INWT	TG	rs132813094	A/C	1	7	33	0.0432	0.0670
INWT	TG	rs386026054	G/C	3	24	12	0.0022	0.0053
HRVWT[2]	CAST	rs109702795	G/T	0	10	29	0.0291	0.2385
HRVWT	CAST	rs110136749	G/A	0	16	24	0.0509	0.1410
HRVWT	CAST	rs110374623	T/C	0	10	28	0.0415	0.1796
HRVWT	CAST	rs133120980	C/A	0	10	31	0.0376	0.1721
HRVWT	CAST	rs133891017	A/T	0	10	30	0.0376	0.1721
HRVWT	CAST	rs134030456	C/T	0	15	26	0.0413	0.1563
HRVWT	CAST	rs136875549	T/C	0	15	24	0.0472	0.1229
HRVWT	CAST	rs137371179	T/C	0	12	29	0.0310	0.1967
HRVWT	CAST	rs137601357	C/T	0	17	24	0.0533	0.1377
HRVWT	CAST	rs137726884	A/G	0	8	29	0.0330	0.1643
DOF[3]	CAST	rs110496242	G/A	2	10	29	0.0362	0.1574
ADG[4]	TG	rs136849694	G/A	3	0	5	0.0054	0.0229
ADG	ADIPOQ	rs210607551	C/T	0	5	36	0.0430	0.7253

[1]Feedlot entrance weight
[2]Harvest weight
[3]Days on feed
[4]Average daily gain
[5]Minor allele represented on the left
[6]Number of animals inheriting each gene

(rs109122904) showed animals inheriting the heterozygous genotype exhibited heavier INWT than the animals inheriting the major allele genotype. When evaluating the seven SNP associated with feedlot entrance weight located on the TG gene, a variety of genotypic effects were observed (Table 4.10). Analyses revealed that animals inheriting the minor allele genotype from four SNP located on the TG gene (rs110501231,

rs133980693, rs386026054, and rs135059985) had significantly heavier INWT than animals inheriting either the heterozygous or major allele genotypes. There was also a significant difference in INWT seen between the heterozygotes and animals with the major allele genotype. Markers rs378567477 and rs132813094 on the TG gene showed individuals inheriting the major allele genotypes had significantly heavier INWT than both heterozygous and minor allele genotype individuals. Alternately, TG marker rs110553649 showed individuals inheriting the minor allele genotype had significantly heavier INWT than individuals inheriting the heterozygous or major allele genotypes. Five SNP located on the GH1 gene (rs133403174, rs133438805, rs134389836, rs136132855, and rs137252133) were significantly associated with feedlot entrance weight (Table 4.10). A significant ($p<.05$) difference was seen between the lighter INWT of the heterozygotes and the heavier INWT of the major allele genotype animals, however both the major allele animals and the heterozygotes were not significantly different from the INWT of the minor allele genotypes.

A total of ten SNP markers were significantly associated with HRVWT. All ten markers (rs109702795, rs110136749, rs110374623, rs133120980, rs133891017, rs134030456, rs136875549, rs137371179, rs137601357, and rs137726884) were located on the CAST gene exhibited similar effects on HRVWT. Animals inheriting heterozygous genotypes for all ten markers resulted in significantly heavier HRVWT than animals inheriting the major allele genotypes. (Table 4.10)

A single SNP located on the CAST gene was significantly associated ($P< .05$) with days on feed (DOF; Table 4.10). Specifically, animals inheriting the minor allele genotype for SNP rs110496242, had significantly increased number of days on feed as compared to animals inheriting the major allele genotype. There was not a significant difference seen, however, in the comparison of the number of days on feed between the heterozygous genotype and either of the homozygous genotypes.

Table 4.10: Single nucleotide polymorphisms associated with feedlot traits and least square means estimate comparisons between reported genotypes. Differing superscripts indicate a difference of means at P<0.05 within rows.

Traits	Gene	SNP ID	Allele[5]	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
INWT[1]	IGF-1	rs109022910	A/G	587.98±44.85^{a}	503.27±33.54^{b}	479.25±29.57^{b}
INWT	IGF-1	rs109227434	T/C		505.71±23.38^{a}	412.34±31.68^{b}
INWT	CAST	rs110496242	G/A	458.79±49.98^{a}	386.23±45.10^{b}	489.56±29.89^{a}
INWT	CAST	rs137265200	C/T		534.21±34.34^{a}	476.86±30.59^{b}
INWT	CAPN3	rs109122904	A/G		593.13±42.18^{a}	482.04±29.11^{b}
INWT	TG	rs110501231	C/T	617.04±34.57^{a}	498.79±21.58^{b}	417.35±32.26^{c}
INWT	TG	rs133980693	G/A	617.04±34.57^{a}	498.79±21.58^{b}	417.35±32.26^{c}
INWT	TG	rs378567477	T/C	421.36±34.61^{a}	501.23±24.25^{a}	617.54±36.84^{b}
INWT	TG	rs386026054	G/C	631.63±37.45^{a}	498.26±19.68^{b}	416.91±31.33^{c}
INWT	TG	rs135059985	C/T	617.04±34.57^{a}	498.79±21.58^{b}	417.35±32.26^{c}
INWT	TG	rs110553649	A/C	593.18±46.49^{a}	487.77±27.54^{b}	475.19±30.03^{b}
INWT	TG	rs132813094	A/C	375.29±58.74^{a}	395.87±46.91^{a}	489.41±30.18^{b}
INWT	GH-1	rs133403174	G/A	423.24±46.98^{ab}	408.68±32.05^{a}	509.57±19.82^{b}
INWT	GH-1	rs133438805	G/C	423.24±46.98^{ab}	408.68±32.05^{a}	509.57±19.82^{b}
INWT	GH-1	rs134389836	C/T	423.24±46.98^{ab}	408.68±32.05^{a}	509.57±19.82^{b}
INWT	GH-1	rs136132855	T/C	423.24±46.98^{ab}	408.68±32.05^{a}	509.57±19.82^{b}
INWT	GH-1	rs137252133	A/G	423.24±46.98^{ab}	408.68±32.05^{a}	509.57±19.82^{b}
HRVWT[2]	CAST	rs109702795	G/T		649.66±30.67^{a}	593.26±21.80^{b}
HRVWT	CAST	rs110136749	G/A		650.14±22.51^{a}	580.39±17.39^{b}
HRVWT	CAST	rs110374623	T/C		656.81±23.85^{a}	582.58±17.48^{b}
HRVWT	CAST	rs133120980	C/A		656.65±23.34^{a}	581.58±16.78^{b}
HRVWT	CAST	rs133891017	A/T		656.65±23.34^{a}	578.20±17.62^{b}
HRVWT	CAST	rs134030456	C/T		653.39±23.08^{a}	581.04±17.49^{b}
HRVWT	CAST	rs136875549	T/C		651.24±23.68^{a}	591.25±21.78^{b}
HRVWT	CAST	rs137371179	T/C		645.35±30.12^{a}	580.26±17.56^{b}
HRVWT	CAST	rs137601357	C/T		649.25±22.57^{a}	580.45±17.57^{b}
HRVWT	CAST	rs137726884	A/G		658.68±24.43^{a}	582.19±16.65^{b}
DOF[3]	CAST	rs110496242	G/A	310.50±18.78^{a}	282.50±12.83^{ab}	262.88±8.37^{b}
ADG[4]	TG	rs136849694	G/A	0.83±0.09^{a}		1.46±0.07^{b}
ADG	ADIPOQ	rs210607551	C/T		1.36±0.16^{a}	1.19±0.14^{b}

[1]Feedlot entrance weight
[2]Harvest weight
[3]Days on feed
[4]Average daily gain
[5]Minor allele represented on the left

Two markers located on the TG and ADPIOQ genes were identified as having significant effects P value on average daily gain (ADG). Animals inheriting the major allele genotype showed a larger ADG than animals

inheriting the minor allele genotype for marker rs136849694 from the TG gene. Marker rs210607551 from the ADIPOQ showed animals inheriting the heterozygous genotype exhibited a larger ADG than animals inheriting the major allele genotype (Table 4.10).

SNP ASSOCIATED WITH CARCASS TRAITS

When evaluating SNP associations with carcass composition traits hot carcass weight, rib eye area, and yield grade, a significance association (P<.05) was found for a total of 19 SNP with 5 candidate genes represented (TG, CAST, CAPN3, IGF1, and GH1) (Table 4.11).

Three SNP were significantly associated (P< .05) with hot carcass weight (HCW; Table 4.12). Located on the CAST gene, all markers (rs109702795, rs134030456, and rs137371179) exhibited similar results on HCW. Animals inheriting the heterozygous genotypes displayed significantly heavier hot carcass weights when compared to animals inheriting the major allele genotypes.

Fifteen SNP were found to be significantly associated (p<.05) with rib eye area (REA). Single nucleotide polymorphisms from 5 of the candidate genes utilized in the current study were significantly associated with REA. Specifically, six SNP located on the CAST gene, one SNP located on the IGF1 gene, two located on the CAPN3 gene, five located on the TG gene, and one located on the GH1 gene. Analysis of SNP located on the CAST gene (rs109020860, rs110386026, rs136873074, rs136882857, rs136982429, and rs137561617) revealed animals inheriting the heterozygous genotype displayed significantly larger REA than animals inheriting the major allele genotype. An SNP located on the IGF1 gene (rs109022910) showed animals inheriting the minor allele genotype displayed significantly larger REA than animals inheriting the heterozygous or minor allele genotypes. Two markers located on the CAPN3 gene (rs109122904, rs137651874) showed significant associations with REA. Individuals inheriting the heterozygous genotype for rs109122904 showed larger REA than animals inheriting the major allele genotype, and CAPN3 marker rs110452450 revealed animals inheriting the heterozygous or major allele genotypes displayed larger REA than animals

Table 4.11: Level of significance and frequency of animals from each genotype associated with carcass composition traits

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Frequency[5]	Het Genotype Frequency[5]	Major Genotype Frequency[5]	SNP P-value	Breed P-value
HCW[1]	CAST	rs109702795	G/T	0	10	29	0.0303	0.2473
HCW	CAST	rs134030456	C/T	0	15	26	0.0544	0.1792
HCW	CAST	rs137371179	T/C	0	12	29	0.0324	0.2117
REA[2]	CAST	rs109020860	A/G	0	5	36	0.0425	0.1612
REA	CAST	rs110386026	C/T	0	6	35	0.0425	0.1612
REA	CAST	rs136873074	C/T	0	6	34	0.0425	0.1753
REA	CAST	rs136882857	C/T	0	6	35	0.0425	0.1612
REA	CAST	rs136982429	C/T	0	11	28	0.0032	0.2548
REA	CAST	rs137561617	T/A	0	6	31	0.0139	0.1775
REA	IGF-1	rs109022910	A/G	4	9	26	0.0459	0.1891
REA	CAPN3	rs109122904	A/G	0	5	36	0.0354	0.1713
REA	CAPN3	rs110452450	G/A	10	13	13	0.0367	0.0025
REA	TG	rs110553649	A/C	2	20	19	0.0333	0.1136
REA	TG	rs110946911	T/G	2	17	22	0.0113	0.2394
REA	TG	rs132813094	A/C	1	7	33	0.0400	0.1784
REA	TG	rs134743669	G/A	0	39	2	0.0076	0.1787
REA	TG	rs386026054	G/C	3	24	12	0.0221	0.4712
REA	GH-1	rs137651874	T/C	0	6	29	0.0401	0.3600
YG[3]	CAST	rs134030456	C/T	0	15	26	0.0443	0.1951

[1]Hot carcass weight
[2]Rib eye area
[3]Yield grade
[4]Minor allele represented on the left
[5]Number of animals inheriting each gene

inheriting the minor allele genotype. Analysis of five markers located on the TG gene (rs110553649, rs110946911, rs132813094, rs134743669, and rs386026054) displayed significant association with REA. Analysis of TG markers (rs110946911 and rs386026054) revealed individuals inheriting the minor allele genotypes displayed larger REA than those individuals inheriting the respective heterozygous or major allele genotypes. Similarly, TG marker rs134743669 revealed individuals inheriting the minor allele genotype showed larger REA than individuals with the heterozygous genotype. Marker rs132813094 located on the TG gene

displayed a significantly larger REA in animals inheriting the minor allele genotype animals when compared with the heterozygous genotype individuals, but no significant difference was seen when comparing the REA of

Table 4.12: Single nucleotide polymorphisms associated with carcass composition traits and least square means estimate comparisons between reported genotypes. Differing superscripts indicate a difference of means at P<0.05 within rows.

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
HCW[1]	CAST	rs109702795	G/T		396.30±20.60[a]	361.85±15.47[b]
HCW	CAST	rs134030456	C/T		401.51±17.97[a]	350.29±13.45[b]
HCW	CAST	rs137371179	T/C		393.32±20.42[a]	359.62±15.67[b]
REA[2]	CAST	rs109020860	A/G		36.68±1.72[a]	33.22±0.98[b]
REA	CAST	rs110386026	C/T		36.68±1.72[a]	33.22±0.98[b]
REA	CAST	rs136873074	C/T		36.81±1.71[a]	33.32±0.96[b]
REA	CAST	rs136882857	C/T		36.68±1.72[a]	33.22±0.98[b]
REA	CAST	rs136982429	C/T		36.03±1.29[a]	32.34±1.08[b]
REA	CAST	rs137561617	T/A		37.26±1.67[a]	33.05±0.90[b]
REA	IGF-1	rs109022910	A/G	37.87±1.60[a]	34.12±1.21[b]	33.19±0.82[b]
REA	CAPN3	rs109122904	A/G		36.88±1.56[a]	33.41±0.84[b]
REA	CAPN3	rs110452450	G/A	30.51±1.44[a]	34.68±0.88[b]	34.84±0.76[b]
REA	TG	rs110553649	A/C	37.45±2.47[a]	32.50±1.41[b]	34.93±1.56[a]
REA	TG	rs110946911	T/G	42.18±2.87[a]	34.49±1.15[b]	32.64±1.01[b]
REA	TG	rs132813094	A/C	37.14±2.76[a]	30.68±1.67[b]	33.42±1.01[ab]
REA	TG	rs134743669	G/A	40.01±2.74[a]	33.32±0.95[b]	
REA	TG	rs386026054	G/C	40.03±2.15[a]	33.18±1.12[b]	32.40±1.79[b]
REA	GH-1	rs137651874	T/C		37.42±1.49[a]	33.48±0.90[b]
YG[3]	CAST	rs134030456	C/T		4.11±0.36[a]	3.10±0.28[b]

[1]Hot carcass weight
[2]Rib eye area
[3]Yield grade
[4] Minor allele represented on the left

the major allele genotype animals with the REA of heterozygotes or minor allele genotype animals. The TG gene marker rs110553649 revealed animals inheriting the heterozygous genotype exhibited significantly smaller REA than either homozygous genotype, and there was no significant difference seen between the REA of the major and minor allele genotypes. Finally for REA, one SNP from the GH1 gene (rs137651874) revealed animals inheriting the heterozygous genotype displayed significantly larger REA than animals inheriting the major allele genotype. (Table 4.12).

One SNP located on the CAST gene was significantly associated (P< .05) with yield grade (YG). Marker rs134030456 on the CAST gene revealed animals inheriting the heterozygous genotype displayed significantly lower yield grade as compared to animals inheriting the major allele genotype (Table 4.12).

When evaluating SNP associations with carcass quality traits marbling score, quality grade, and Warner-Bratzler shear force score, a significance association (P<.05) was found. A total of 30 significant SNP were located on candidate genes TG, ADIPOQ, CAST, CAPN3, IGF1, and GH1 (Table 4.13).

A total of 13 SNP were found to be significantly associated (P<.05) with marbling score (MARB). Single nucleotide polymorphisms from five candidate genes utilized in the current study were significantly associated with marbling score. Specifically, one located on the ADIPOQ gene, one located on the IGF1 gene, two located on the CAPN3 gene, one located on the CAST gene, and eight located on the TG gene (Table 4.14). Analysis of SNP rs383535987 located on the ADIPOQ gene showed individuals with the heterozygous genotype exhibited larger marbling scores than animals inheriting the major allele genotype. One SNP located on IGF1 gene (rs109022910) indicated animals with the minor allele genotype had greater marbling scores than either the heterozygous or major allele genotype animals, with no significant difference seen between the heterozygous and major homozygous genotypes. The significant marker located on the CAST gene (rs110496242) showed animals inheriting the major allele genotype exhibited significantly larger marbling scores than the heterozygous genotype animals. No significant difference was seen in comparing the minor allele genotype with the major or heterozygous genotypes. Two SNP were observed from the CAPN3 gene (rs109050259, rs134085397) Marker rs109050259 indicated animals with the minor allele genotype showed significantly smaller marbling scores than the heterozygous or major allele genotypes, with no significant difference between the heterozygous and major allele genotypes. Alternately for CAPN3 marker rs134085397, animals inheriting the minor allele genotype had significantly larger marbling scores than animals of the major allele genotype, and the animals inheriting the heterozygous genotype did not show significant difference in

Table 4.13: Level of significance and frequency of animals from each genotype associated with carcass quality traits

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Frequency[5]	Het Genotype Frequency[5]	Major Genotype Frequency[5]	SNP P-value	Breed P-value
MARB[1]	IGF-1	rs109022910	A/G	4	9	26	0.0022	0.0005
MARB	CAPN3	rs109050259	G/A	2	23	16	0.0136	0.1924
MARB	CAPN3	rs134085397	G/A	6	21	14	0.0227	0.0948
MARB	CAST	rs110496242	G/A	2	10	29	0.0105	0.1457
MARB	TG	rs109182502	T/C	0	3	38	0.0047	0.0166
MARB	TG	rs110501231	C/T	9	22	10	<0.0001	0.0127
MARB	TG	rs110553649	A/C	2	20	19	0.0492	0.2080
MARB	TG	rs386026054	G/C	3	24	12	0.0029	0.0017
MARB	TG	rs133980693	G/A	9	22	10	<0.0001	0.0127
MARB	TG	rs135059985	C/T	9	22	10	<0.0001	0.0127
MARB	TG	rs378567477	T/C	8	16	9	0.0007	0.0839
MARB	TG	rs378900777	T/C	0	2	39	0.0504	0.1321
MARB	ADIPOQ	rs383535987	G/A	0	3	38	0.0039	<0.0001
QG[2]	IGF-1	rs109022910	A/G	4	9	26	0.0286	0.0016
QG	CAPN3	rs109050259	G/A	2	23	16	0.0009	0.2217
QG	CAST	rs110496242	G/A	2	10	29	0.0003	0.0412
QG	TG	rs109182502	T/C	0	3	38	0.0235	0.0098
QG	TG	rs110501231	C/T	9	22	10	0.0020	0.0176
QG	TG	rs132813094	A/C	1	7	33	0.0416	<0.0001
QG	TG	rs386026054	G/C	3	24	12	0.0311	0.0047
QG	TG	rs133980693	G/A	9	22	10	0.0020	0.0176
QG	TG	rs135059985	C/T	9	22	10	0.0020	0.0176
QG	TG	rs378567477	T/C	8	16	9	0.0124	0.1284
QG	GH-1	rs137651874	T/C	0	6	29	0.0218	0.0007
QG	ADIPOQ	rs380209068	G/A	0	3	36	0.0363	<0.0001
QG	ADIPOQ	rs383535987	G/A	0	3	38	0.0199	<0.0001
QG	ADIPOQ	rs384076273	T/C	0	4	37	0.0556	<0.0001
WBS[3]	IGF-1	rs110959643	A/G	0	2	39	0.0537	0.3198
WBS	CAST	rs137140434	G/T	0	5	13	0.0431	0.7612
WBS	ADIPOQ	rs383535987	G/A	0	3	38	0.0293	0.3788

[1]Marbling
[2]Quality grade
[3]Warner-Bratzler shear force
[4]Minor allele represented on the left
[5]Number of animals inheriting each gene

MARB than animals of either homozygous genotype. When evaluating the eight SNP associated with MARB located on the TG gene, a variety of genotypic effects were observed. Individuals inheriting the heterozygous genotype for rs109182502 and rs378900777 had higher marbling scores than those individuals inheriting the respective major allele genotypes. For marker rs386026054 on the TG gene, individuals inheriting the minor

Table 4.14: Single nucleotide polymorphisms associated with carcass quality traits and least square means estimate comparisons between reported genotypes. Differing superscripts indicate a difference of means at P<0.05 within rows.

Traits	Gene	SNP ID	Allele[4]	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
MARB[1]	ADIPOQ	rs383535987	G/A		560.00±37.70^{a}	437.05±12.06^{b}
MARB	IGF-1	rs109022910	A/G	565.00±31.66^{a}	457.08±24.18^{b}	426.56±16.01^{b}
MARB	CAPN3	rs109050259	G/A	285.91±50.09^{a}	422.02±23.75^{b}	440.23±23.94^{b}
MARB	CAPN3	rs134085397	G/A	491.66±29.14^{a}	435.56±20.71^{ab}	395.45±24.39^{b}
MARB	CAST	rs110496242	G/A	372.26±48.60^{ab}	335.12±32.79^{b}	441.65±21.33^{a}
MARB	TG	rs109182502	T/C		525.46±38.54^{a}	420.27±21.79^{b}
MARB	TG	rs110501231	C/T	547.50±21.59^{a}	433.15±16.07^{b}	371.11±32.19^{b}
MARB	TG	rs110553649	A/C	558.29±47.64^{a}	444.45±15.65^{b}	416.19±25.54^{b}
MARB	TG	rs133980693	G/A	547.50±21.60^{a}	433.15±16.07^{b}	371.11±32.19^{b}
MARB	TG	rs135059985	C/T	547.50±21.60^{a}	433.15±16.07^{b}	371.11±32.19^{b}
MARB	TG	rs378567477	T/C	372.86±34.61^{a}	446.11±21.58^{a}	547.50±22.89^{b}
MARB	TG	rs378900777	T/C		529.80±48.85^{a}	431.69±16.95^{b}
MARB	TG	rs386026054	G/C	553.33±36.01^{a}	443.33±14.23^{b}	369.50±32.71^{c}
QG[2]	IGF-1	rs109022910	A/G	755.00±19.20^{a}	703.29±14.76^{b}	694.06±9.71^{b}
QG	CAPN3	rs109050259	G/A	595.66±24.70^{a}	699.39±9.16^{b}	704.22±9.43^{b}
QG	CAST	rs110496242	G/A	668.14±24.91^{ab}	637.81±13.62^{a}	706.94±8.20^{b}
QG	TG	rs109182502	T/C		747.65±21.76^{a}	695.10±7.89^{b}
QG	TG	rs110501231	C/T	749.25±13.02^{a}	696.35±9.69^{b}	670.39±19.41^{b}
QG	TG	rs386026054	G/C	751.00±21.83^{a}	701.08±8.63^{b}	668.85±19.83^{b}
QG	TG	rs132813094	A/C	680.00±38.18^{ab}	656.33±15.59^{b}	701.36±7.10^{a}
QG	TG	rs133980693	G/A	749.25±13.02^{a}	696.35±9.69^{b}	670.39±19.41^{b}
QG	TG	rs135059985	C/T	749.25±13.02^{a}	696.35±9.69^{b}	670.39±19.41^{b}
QG	TG	rs378567477	T/C	671.93±21.56^{a}	701.94±13.45^{a}	749.25±14.26^{b}
QG	GH-1	rs137651874	T/C		742.83±16.17^{a}	798.64±8.42^{b}
QG	ADIPOQ	rs380209068	G/A		649.00±22.20^{a}	700.01±7.09^{b}
QG	ADIPOQ	rs383535987	G/A		753.33±21.60^{a}	697.82±6.91^{b}
QG	ADIPOQ	rs384076273	T/C		655.67±21.81^{a}	700.92±6.65^{b}
WBS[3]	IGF-1	rs110959643	A/G		9.92±1.13^{a}	7.79±0.50^{b}
WBS	CAST	rs137140434	G/T		5.99±0.61^{a}	7.62±0.38^{b}
WBS	ADIPOQ	rs383535987	G/A		5.66±1.10^{a}	8.00±0.54^{b}

[1]Marbling score
[2]Quality grade
[3]Warner-Bratzler shear force
[4] Minor allele represented on the left

allele genotype displayed larger marbling scores than the heterozygous or major allele genotypes. Also, animals inheriting the heterozygous genotype showed significant increase in marbling score as compared to the major allele genotype. Marker rs378567477 from the TG gene indicated animals inheriting the minor allele showed

significantly smaller marbling scores than animals inheriting the major allele genotype. The final four TG markers rs110501231, rs110553649, rs133980693, and rs135059985 indicated animals inheriting the respective minor allele genotypes showed significantly larger marbling scores than animals inheriting the respective heterozygous genotypes or the major allele genotypes. (Table 4.14)

A total of 14 SNP were found to be significantly associated ($P<.05$) with quality grade (QG). All six candidate genes were represented with the frequency of one marker from each IGF1, CAPN3, CAST, and GH1, three markers from ADIPOQ, and seven markers from TG (Table 4.14). The marker from IGF1 (rs109022910) showed animals inheriting the minor allele genotype exhibited better quality grade scores than animals of either the heterozygous or major allele genotypes, and no significant effect was seen between QG of heterozygous and major allele genotype animals. Alternately, the CAPN3 marker (rs109050259) showed animals inheriting the minor allele genotype had lower QG scores than animals inheriting the heterozygous or major allele genotypes, with no significance seen between QG of the major allele genotypes and heterozygous genotypes. The SNP from the CAST gene rs110496242 indicated animals inheriting the major allele genotype showed significantly higher QG than animals inheriting the heterozygous genotype. No significant difference was seen, however, when comparing the QG of the minor allele genotype with the QG of the heterozygous or major allele genotypes. Marker rs137651874 from the GH1 candidate gene indicated a significant increase in QG for animals inheriting the major allele genotypes as compared to animals with the heterozygous genotypes. Two of the three markers from the ADIPOQ candidate gene (rs380209068 and rs384076273) indicated a significant increase in QG for animals inheriting the respective major allele genotypes as compared to animals with the heterozygous genotypes. The third marker from the ADIPOQ gene (rs383535987) indicated animals with the heterozygous genotype showed a larger QG score than did the heirs of the major allele genotype. When evaluating the seven SNP associated with QG located on the TG gene, a variety of genotypic effects were observed. Individuals inheriting the heterozygous genotype for rs109182502 had higher QG scores than those

individuals inheriting the major allele genotype. Individuals inheriting the minor allele genotype for rs110501231, rs386026054, rs133980693, and rs135059985 had higher QG scores than those individuals inheriting the respective major alleles in their genotypes. No significant difference was realized when comparing heterozygous and the respective major allele genotypes for these four markers. Marker rs378567477 on the TG gene revealed animals with the significantly higher QG inherited the major allele genotype, with no significance seen in comparing the heterozygotes with the minor allele homozygotes. Finally, TG marker rs132813094 showed animals with the major allele genotype had greater QG scores than animals with the heterozygous genotype but had no significant difference compared to the minor allele genotype. The minor allele genotype also showed no significant difference when compared to the heterozygous genotype. (Table 4.14)

Three markers from the candidate genes IGF1, CAST, and ADIPOQ were represented as having a significant effect with Warner-Bratzler shear force scores (WBS). Marker rs110959643 from the IGF1 gene indicated a significantly higher shear force score for individuals inheriting the heterozygous genotype. Alternately, marker rs137140434 from the CAST gene and marker rs383535987 from the ADIPOQ gene indicated a significantly lower shear force score for heterozygote individuals when compared to those inheriting the respective major allele genotypes. (Table 4.14)

Discussion

Several thyroglobulin (TG) markers were significantly associated ($P<.05$) with growth traits, feedlot performance, and carcass traits. Specifically, these traits include birth weight, weaning weight, feedlot entrance weight, average daily gain, rib eye area, marbling score, and quality grade. Limited reports have been found associating candidate gene TG with growth traits and feedlot performance in Brahman cattle. Thus the identification of SNP located on the TG gene with birth weight, weaning weight, and feedlot entrance weight in the current study may be novel and should be further investigated. Average daily gain was previously described

to have no association detected with markers on TG gene (Casas et al., 2005), conflicting with the current study. Rib eye area has previously been significantly associated with SNP in TG (Casas et al., 2005). Previous studies have conflicted in reports of favorable alleles located on the TG gene affecting marbling in *Bos indicus* and *Bos taurus* cattle (Casas et al., 2005; van Enennaam et al., 2007; Barendse et al., 1999). One study assessing SNP effects on carcass composition in *Bos indicus* cattle suggested the use of molecular marker information developed in *Bos taurus* populations may require further development of appropriate markers for use in *Bos indicus* populations (Casas et al, 2005).

Adiponectin (ADIPOQ) markers in this study were significantly associated with growth and carcass traits including birth weight, weaning weight, hip height, average daily gain, marbling, quality grade, Warner-Bratzler shear force scoresThis is in agreement with previous studies that have reported an association between ADIPOQ and cattle growth traits such as birth weight, weaning weight, and hip height (Zhang et al.2013). An association between ADIPOQ with carcass traits such as rib eye area, marbling, and backfat thickness has previously been reported (Shin and Chung, 2013; Morsci et al., 2006) which is in agreement with this study for rib eye area and marbling.

Several CAST markers were found to be significantly associated with growth and carcass traits. Specifially, SNP were identified in the current study with weaning weight, hip height, feedlot entrance weight, days on feed, harvest weight, hot carcass weight, ribeye area, yield grade, quality grade, and Warner-Bratzler shear force score. Previous studies have reported CAST SNP associations with tenderness in beef cattle (Smith et al., 2009; Schenkel et al., 206; Café et al., 2010). Smith and associates (2009) reported an association with CAST markers and tenderness in Brahman cattle. Schenkel and associates (2006) reported a higher frequency of favorable CAST allele ‘A’ resulted in lower percentage of tough steaks, higher fat content, and a difference in ribeye area. Café and associates (2010) reported lower shear force scores in steaks from Brahman cattle inheriting the favorable allele. While extensive evaluation have been conducted with the CAST gene and meat

tenderness, little has been reported about the CAST genes association with other economically important traits (Pintos et al., 2011). Markers reported in this study to be associated with growth traits are novel and should be reevaluated with a larger, more diverse population to validate their significance in the current study.

Multiple CAPN3 markers were significantly associated (P<.05) with growth traits and carcass traits. Specifically, multiple SNP were associated with the traits of weaning weight, hip height, feedlot entrance weight, rib eye area, marbling, and quality grade. A particular SNP of interest was associated with days on feed, marbling score, and quality grade score. Café and associates (2010) reported an increase in the frequency of the favorable 'G' allele increases meat tenderness. This is in agreement with the current study.

Analyses revealed that three IGF1 gene SNP were significantly associated (P<.05) with growth traits, feedlot performance, and carcass traits. Specifically, these markers (rs109022910, rs109227434, and rs110959643) were significantly associated with weaning weight, feedlot entrance weight, rib eye area, marbling, quality grade, and Warner-Bratzler shear force score. Previous studies report IGF1 SNP were associated with growth and production traits (Pereira et al., 2005; Machado et al., 2003; Chang et al., 2009). However, marker rs110959643 with an A/G substitution is of particular interest because it has not been previously reported to affect tenderness and/or shear force. Chang and associates (2009) reported significance between IGF1 and carcass weight, but no significance between IGF1 and tenderness. Thus the identification of SNP located on the IGF-1 gene with tenderness in the current study is novel and should be further investigated.

GH1 markers rs133438805, rs134389836, rs133403174, rs137252133, and rs136132855 were found to be significantly associated (P<.05) with feedlot entrance weight. The SNP located on the GH1 gene (rs137651874) was significantly associated with weaning weight, ribeye area, and quality grade. This is in agreement with previous studies that report GH1 is a favorable candidate gene for cattle growth traits and carcass traits (Pereira et al., 2005; Mullen et al., 2010). Pereira and associates (2005) reported a significant effect on yearling weight without risking an increase in birth weight and decrease in calving ease. Marker

rs137651874 is of particular interest as it was found to have a significant effect on rib eye area, as the authors did not find any literature previously suggesting this marker as an indicator for ribeye area and quality grade. Thus the identification of SNP located on the GH1 gene with rib eye area in the current study is novel and should be further investigated.

This objective of the current study was to identify SNP from six candidate genes for possible significant association with farm growth, feedlot performance, and carcass traits. The SNP identified in the current study should be further analyzed to validate the significant associations observed herein. Analysis should be performed with a larger, more diverse population with more locations and environments represented to further confirm possible significant associations with economically important growth and carcass traits such as those reported here.

CHAPTER V
SUMMARY

The Carcass Evaluation Program founded by the American Brahman Breeders Association has produced 10 years of data for evaluation of genetic trends in rate of change for economically important growth and carcass traits in Brahman and Brahman influenced steers. Upon interpretation of the data from 2004-2013, Brahman cattle have shown improvement in the feedlot traits harvest weight (HRVWT) and average daily gain (ADG). These Brahman cattle have also shown improvement in hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), yield grade (YG), quality grade (QG), and dressing percent (DP). An improvement was not seen in Warner-Bratzler shear force score (WBS) overall, but it is to be noted that shear force score has been on a favorable downward trend since 2009.

Utilization of candidate genes for SNP association analysis on Brahman and Brahman influenced steers that completed the Carcass Evaluation Program identified several markers significantly associated with growth and carcass traits. Candidate genes Thyroglobulin (TG), Adiponectin (ADIPOQ), Calpain 3 (CAPN3), Calpastatin (CAST), Insulin like Growth Factor 1 (IGF1), and Growth Hormone gene (GH1) were chosen for previously reported associations with growth and carcass traits of economic importance (Mullen et al., 2010; Pereira et al., 2005; Machado et al., 2003; Casas et al., 2005; Schenkel et al., 2006; Koohmaraie et al., 2002; Barendse et al., 1999). Within the study, analysis revealed representation of all six candidate genes in the 41 SNP found to have 58 significant associations ($p<.05$) with growth and feedlot traits BW, WW, HH, INWT, HRVWT, DOF, and ADG. Furthermore, all six candidate genes were represented in the 32 SNP found to have 49 significant associations with carcass composition and quality traits HCW, REA, YG, MARB, QG, and WBS. No markers showed association with DP. . The SNP identified here should be further analyzed to validate these significant associations. Analysis should be performed with a larger, more diverse population to further confirm

possible significant associations with economically important growth and carcass traits such as those reported here.

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APPENDIX A: DNA EXTRACTION – SATURATED SALT PROCEDURE

Based on extraction procedures described in Miller et al., 1998. Nucl. Acids Res. 16: 1215.

Day 1: in 15ml centrifuge tube

Add: 10-12 ml Lysis buffer (Appendix B) to 250 L white blood cell buffy coat; invert to mix

Spin: 7000rpm for 10 minutes at 4˚C; aspirate supernatant from pellet

Add: 3ml Digestion Buffer (Appendix B); shake vigorously to resuspend pellet

Add: 200µl 1 % SDS and 60µL RNase A (10 mg/ml); invert to mix; incubate for 1 hr at 37˚C with gentle shaking

Add: 25µl Proteinase K (20 mg/ml); invert to mix; incubate overnight at 37˚C with gentle shaking

Day 2:

Add: 1ml Saturated NaCl; Shake vigorously by hand for 15 seconds

Spin: 2800rpm for 30 min at 4˚C; transfer supernatant to new 15ml tube

Add: 2 volumes of 100% Ethanol (stored in freezer); invert gently to mix

Remove: DNA with soft pipette; transfer DNA into 1.5ml snap-cap-tube

Spin: at 10 setting for 10 min in refrigerated bench-top centrifuge; aspirate off most ethanol

Add: 1ml of 80% ethanol (kept on ice); vortex for 20 seconds; spin 5 min in refrigerated bench-top centrifuge; aspirate off most of ethanol

Add: 500µl of 80% ethanol (kept on ice); vortex for 20 seconds; spin 5 min in refrigerated bench-top centrifuge; aspirate off most of ethanol

Leave tubes uncovered to allow pellet to dry overnight

Add: 350µl Rehydration Buffer (Appendix B) to resuspend DNA

Read: on spectrophotometer

APPENDIX B: BUFFER SOLUTION LABORATORY PROTOCOL

LYSIS BUFFER (1L)
7.49g NH_4Cl
2.059g Tris-HCl
pH to 7.4

DIGESTION BUFFER (1L)
1.211g Tris-HCl
23.276g NaCl
0.744g EDTA
pH to 8.0

REHYDRATION BUFFER (1L)
1.21g Tris-HCl
0.37g EDTA

VITA

Amanda Michelle Royer was born March 8 to Butch and Brenda Royer in Baton Rouge, Louisiana. Amanda attended Live Oak High School in Watson, Louisiana where she graduated in May of 2006. She received her Bachelors of Science degree from Louisiana State University A&M College in Animal, Dairy, and Poultry Sciences in December 2011.

Amanda began her Master of Science degree in beef cattle genomics at Louisiana State University with major professor Dr. Matthew D. Garcia in the spring of 2012. Upon completion of her Master of Science degree, she hopes to continue as a contributing member of the beef industry with her own herd of commercial cattle.